8-2007

Relationship Web: Spinning the Semantic Web from Trailblazing to Complex Hypothesis Evaluation

Amit P. Sheth
Wright State University - Main Campus, amit@sc.edu

Relationship Web:

Spinning the Semantic Web from Trailblazing to Complex Hypothesis Evaluation

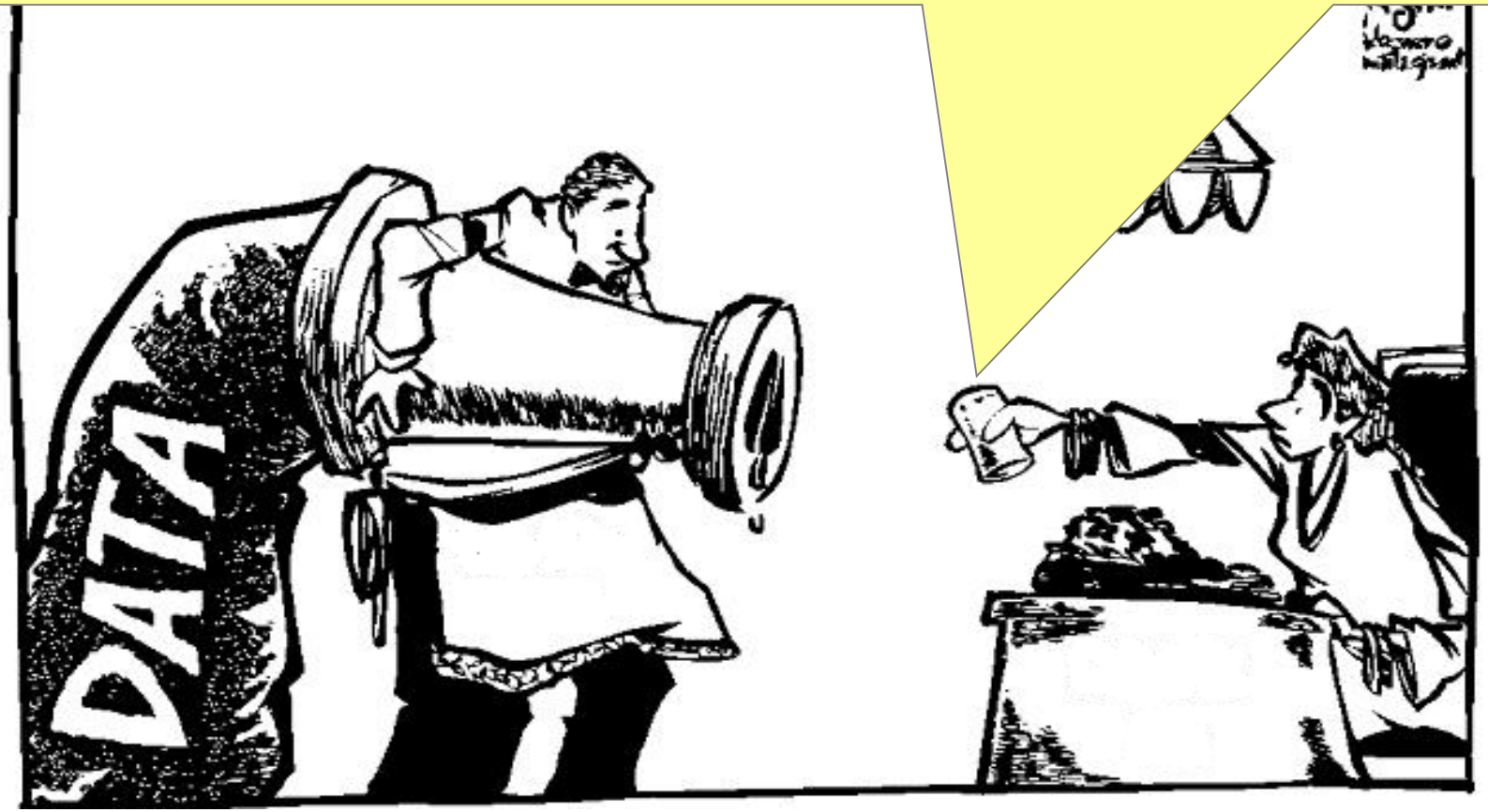
August 2007

Amit Sheth
Kno.e.sis Center, Wright State University,
Dayton, OH

.

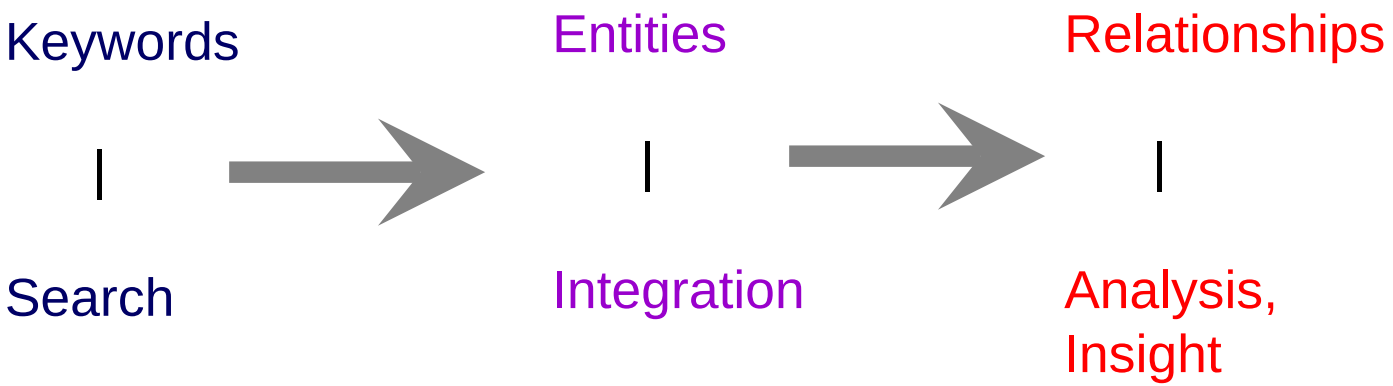
This talk also represents work of several members of Kno.e.sis team, esp. Cartic Ramakrishnan. http://knoesis.wright.edu

Not data (search), but integration, analysis and insight, leading to decisions and discovery



"An object by itself is intensely uninteresting".

Grady Booch, Object Oriented Design with Applications, 1991



Changing the paradigm from document centric to relationship centric view of information

Data captured per year = 1 exabyte (10^{18})
(Eric Neumann, Science, 2005)

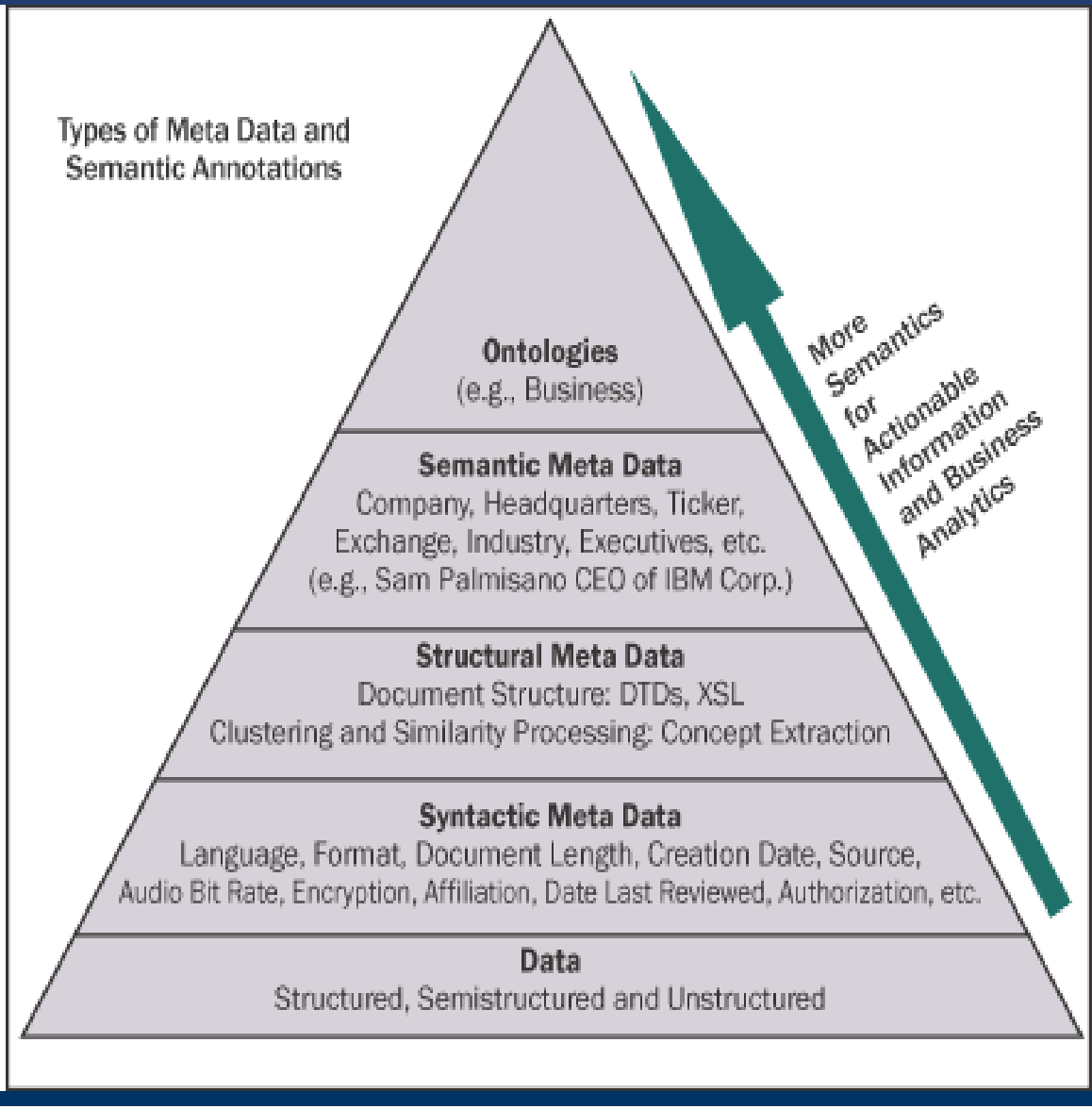
Multiple formats: Structured, unstructured, semi-structured

Multimodal: text, image, a/v, sensor, scientific/engineering

Thematic, Spatial, Temporal

Enterprise to Globally Distributed

Moving from Syntax/Structure to Semantics



Semantics: Meaning & Use of Data

Semantic Web: Labeling data on the Web so both humans and machines can use them more effectively

i.e., Formal, machine processable description ⇨ more automation;

emerging standards/technologies

(RDF, OWL, Rules, ...)

How?

Ontology: Agreement with Common Vocabulary & Domain Knowledge

Semantic Annotation: metadata (manual & automatic metadata extraction)

Reasoning: semantics enabled search, integration, analysis, mining, discovery

Time, Space

Gene Ontology, Glycomics, Proteomics

Pharma Drug, Treatment-Diagnosis

Repertoire Management

Equity Markets

Anti-money Laundering, Financial Risk, Terrorism

Biomedicine is one of the most popular domains in which lots of ontologies have been developed and are in use. See: http://obo.sourceforge.net/browse.html

Clinical/medical domain is also a popular domain for ontology development and applications: http://www.openclinical.org/ontologies.html

is a focused ontology for the description of glycomics

models the biosynthesis, metabolism, and biological relevance of complex glycans

models complex carbohydrates as sets of simpler structures that are connected with rich relationships

An ontology for structure and function of Glycopeptides

Published through the National Center for Biomedical Ontology (NCBO)

More at: http://knoesis.wright.edu/research/bioinformatics/

ProPreO ontology

An ontology for capturing process and lifecycle information related to proteomic experiments

Two aspects of glycoproteomics:

What is it? → identification

How much of it is there? → quantification

Heterogeneity in data generation process, instrumental parameters, formats

Need data and process provenance → ontology-mediated provenance

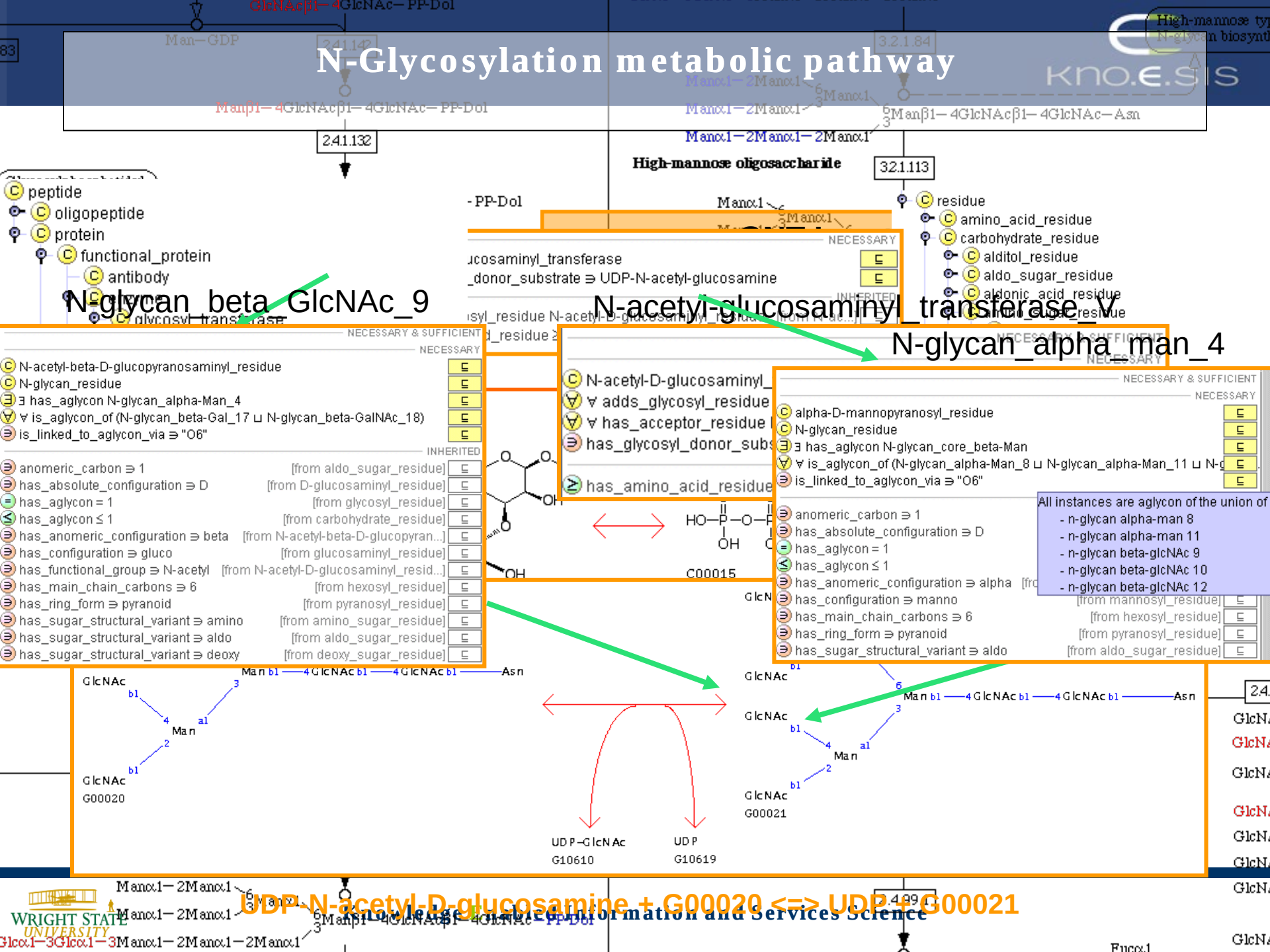
Hence, ProPreO models both the glycoproteomics experimental process and attendant data

Approx 500 classes, 3million+ instances

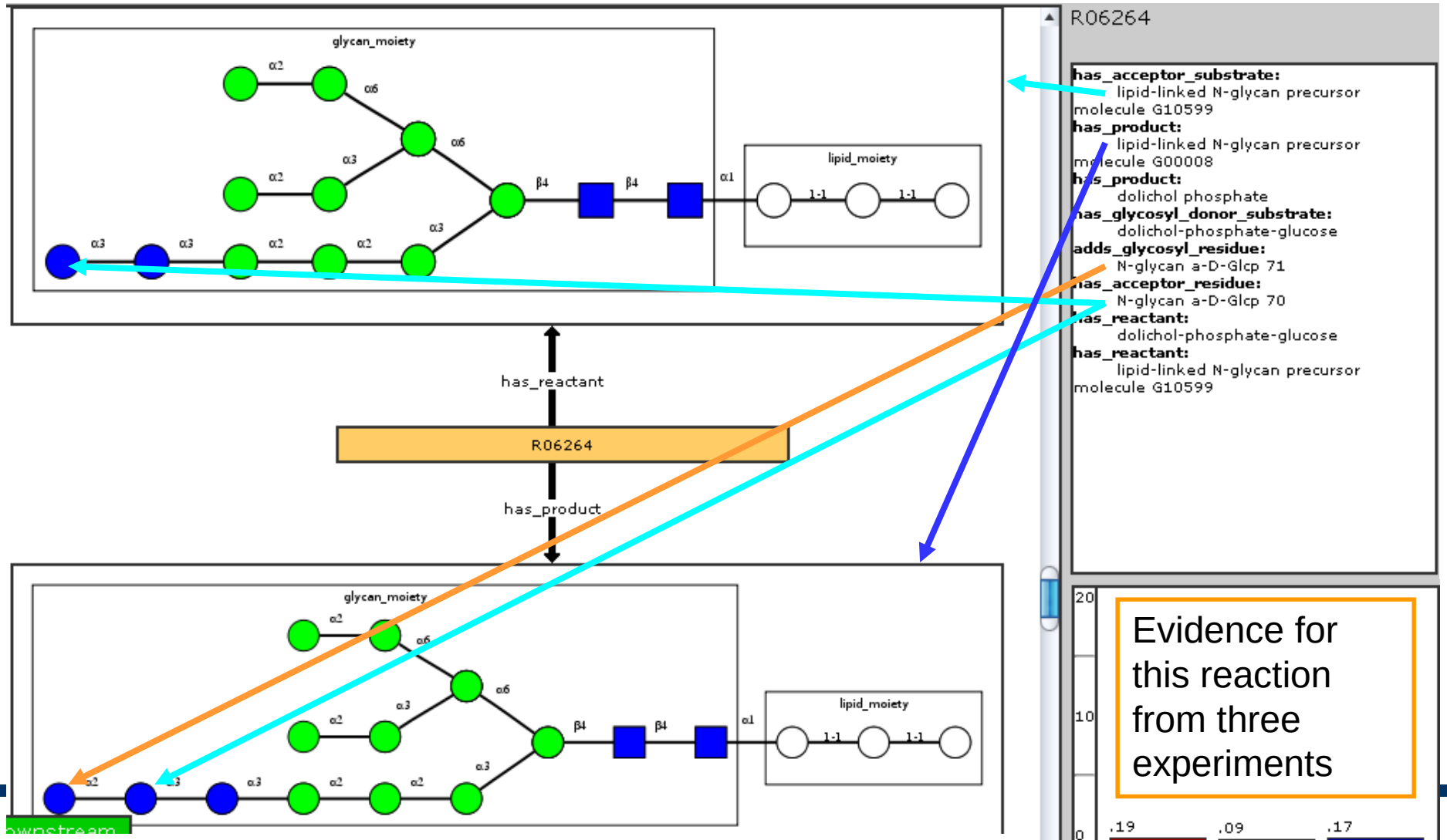
Published through the National Center for Biomedical Ontology (NCBO) and Open Biomedical Ontologies (OBO)

More info. On Knowledge Representation in Life Sciences at Kno.e.sis

N-Glycosylation metabolic pathway

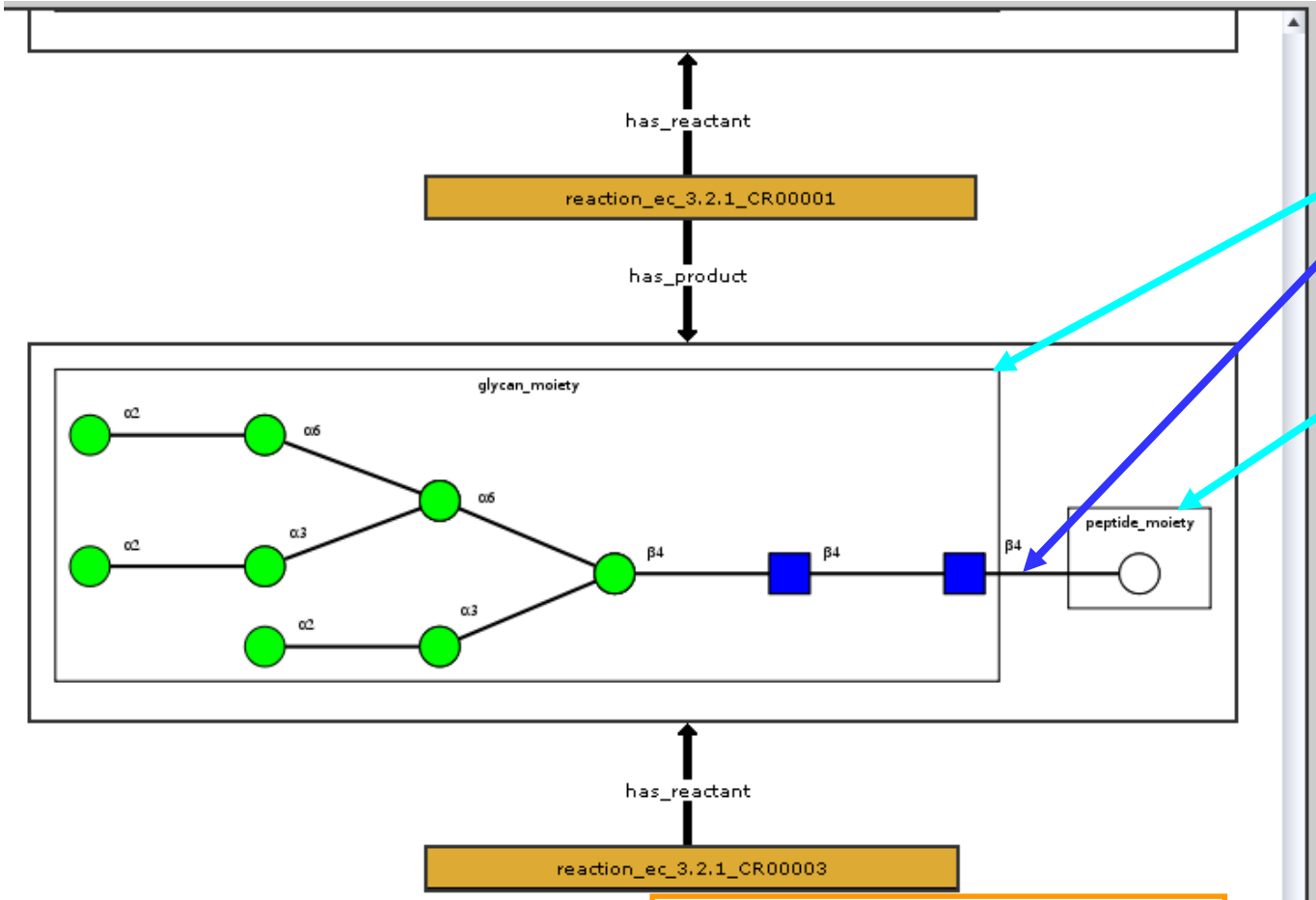


Pathway Steps - Reaction



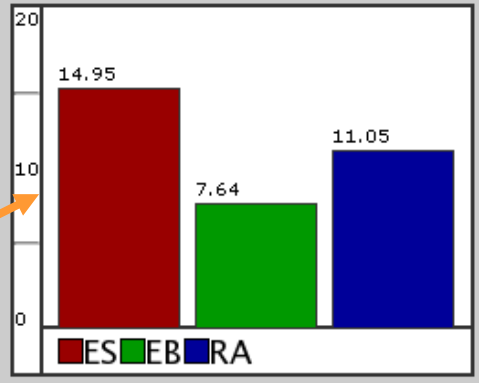
Pathway visualization tool by M. Eavenson and M. Janik, LSDIS Lab, Univ. of Georgia

Pathway Steps - Glycan



glyco peptide G10695

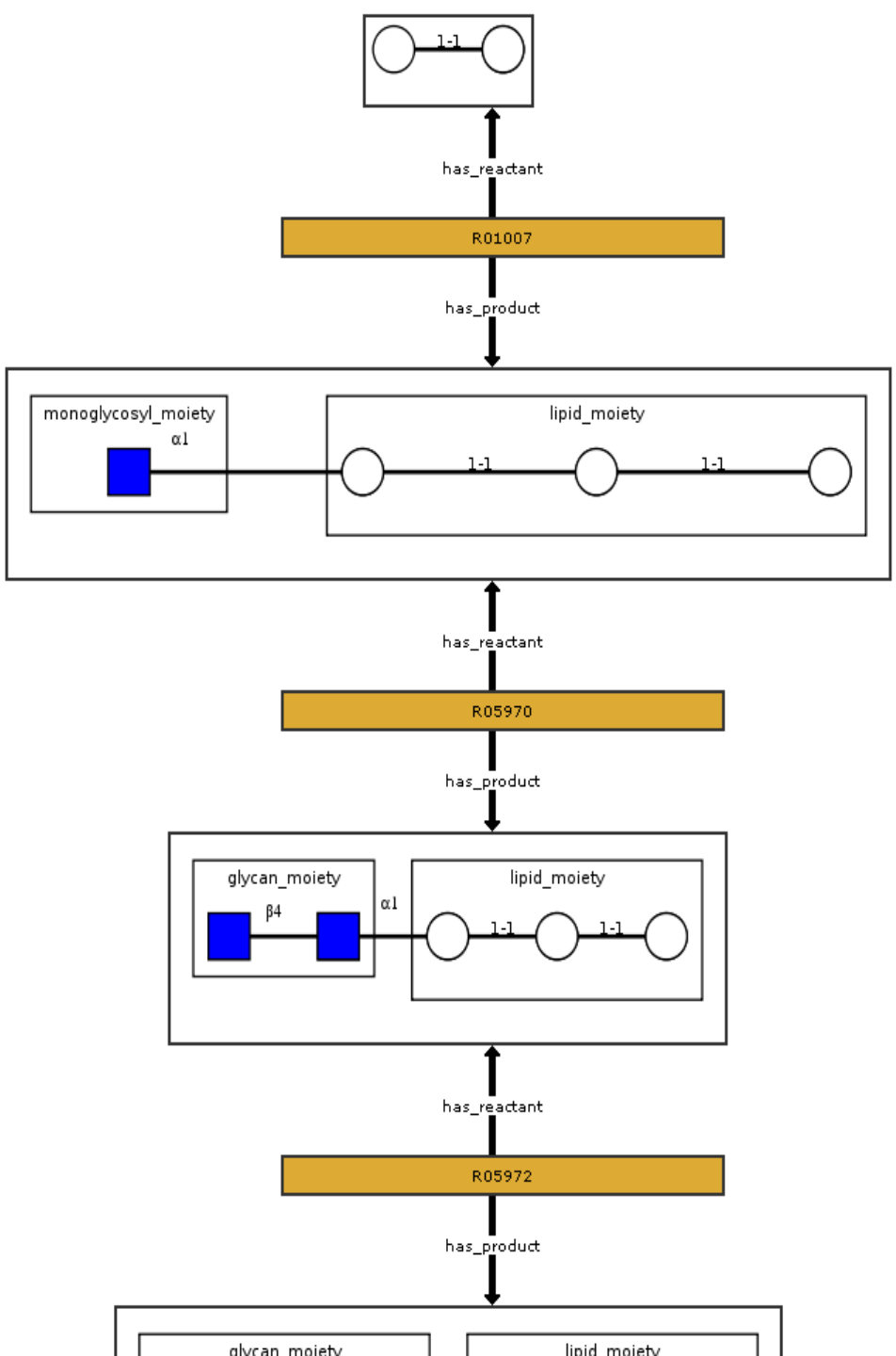
has_peptide_moiety:
representative asparagine-containing peptide moiety
has_carbohydrate_moiety:
N-Glycan-G10695
has_link:
N-glycan precursor moiety G10695 to representative peptide moiety link
label:
G10695
has_moiety:
representative asparagine-containing peptide moiety
has_non-carbohydrate_moiety:
representative asparagine-containing peptide moiety
has_part:
representative asparagine-containing peptide moiety
has_part:
N-Glycan-G10695
has_moiety:
N-Glycan-G10695



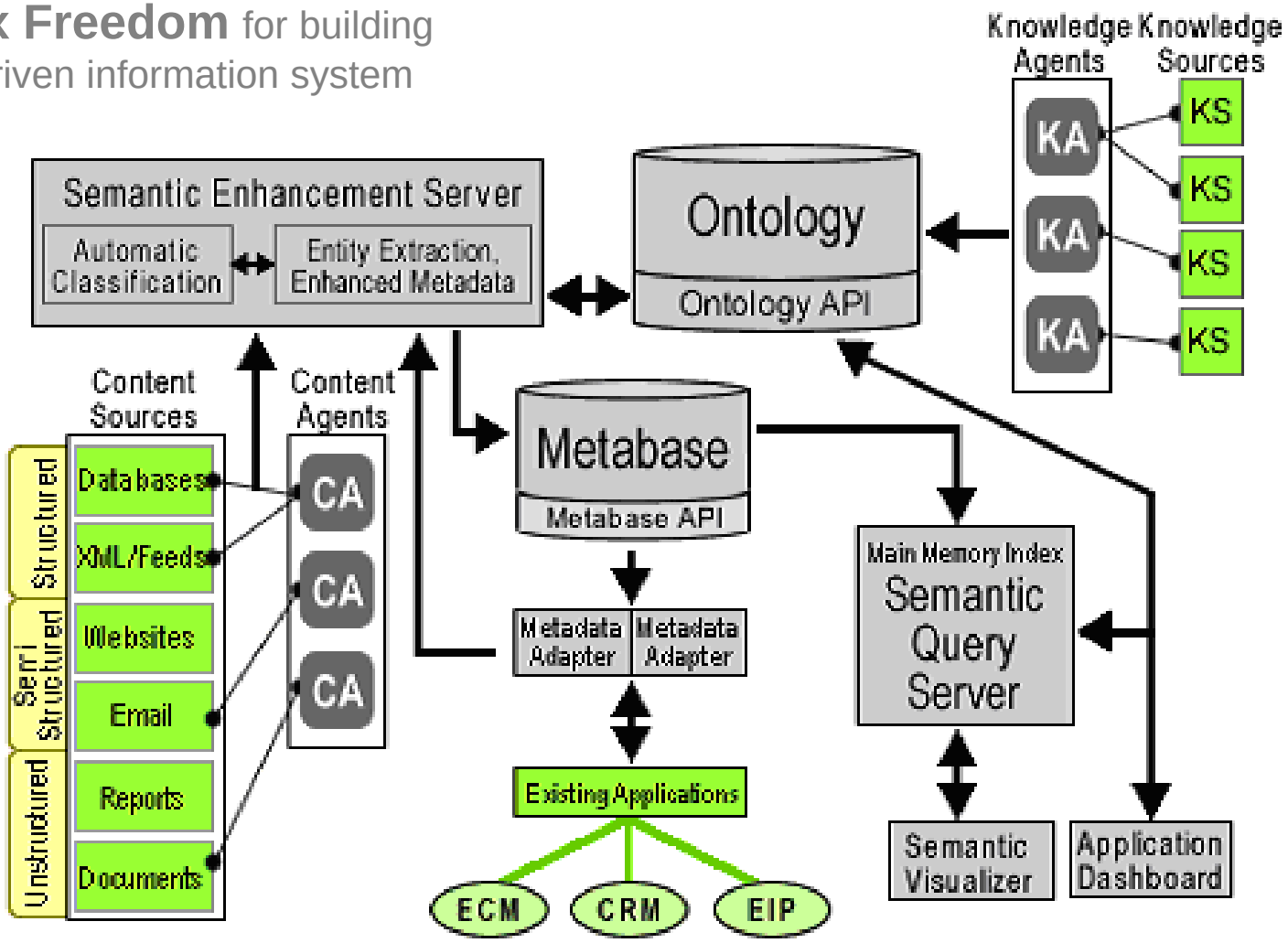
Abundance of this glycan in three experiments

Downstream

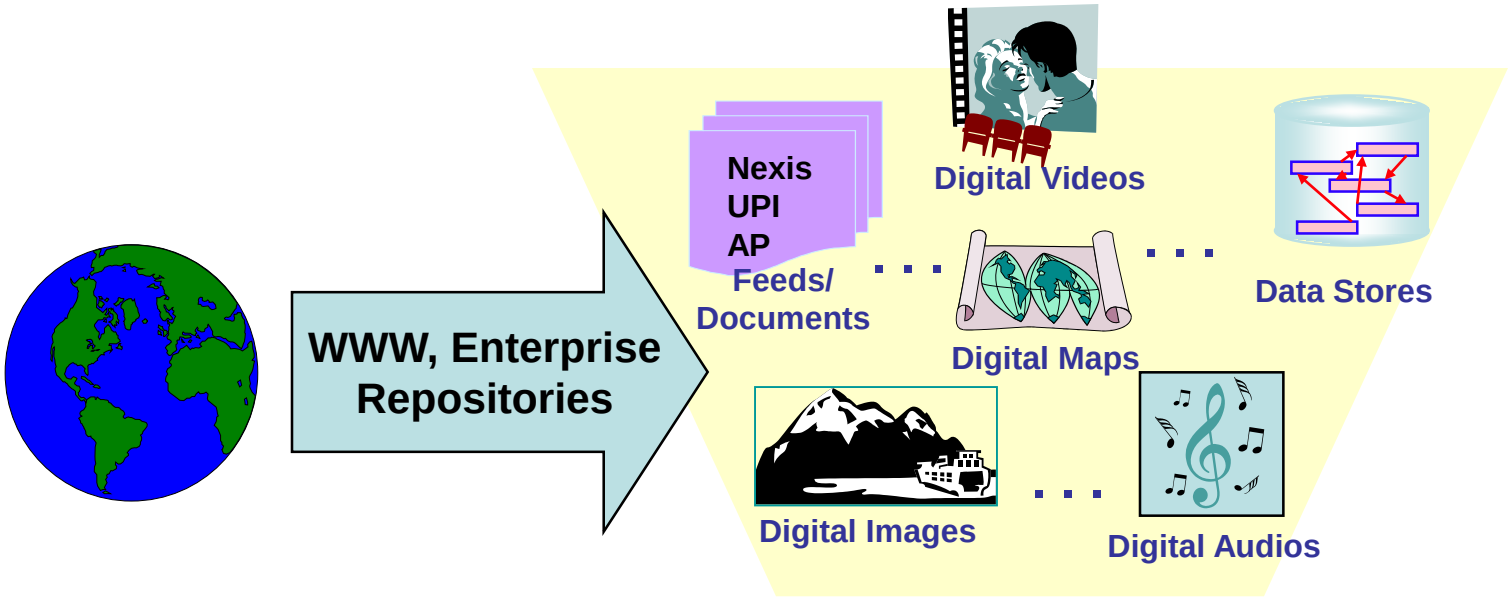
Pathway visualization tool by M. Eavenson and M. Janik, LSDIS Lab, Univ. of Georgia


1-1
has_reactant
R01007
has_product
monoglycosyl_moiety
α1
lipid_moiety
1-1
1-1
has_reactant
R05970
has_product
glycan_moiety
β4
α1
lipid_moiety
1-1
1-1
has_reactant
R05972
has_product
glycan_moiety
lipid_moiety

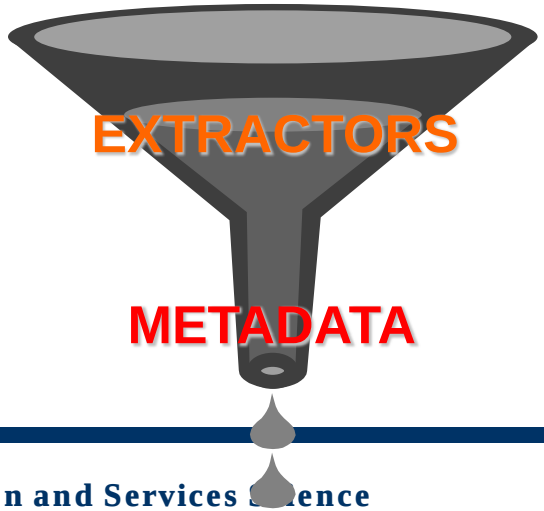
Semagix Freedom for building
ontology-driven information system



Information Extraction for Metadata Creation



Create/extract as much (semantics) metadata automatically as possible



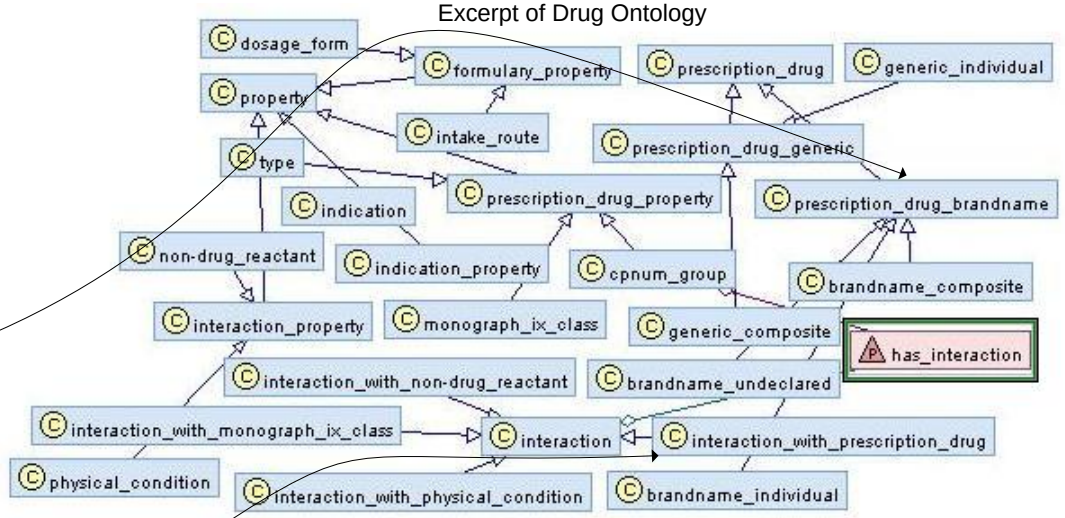
Automatic Semantic Metadata Extraction/Annotation

Semantic Annotation – Elsevier iConsult content

<Entity id="494805" class="DrugOntology#Organization"
Public Health Advisory FDA Announces Important Change
<Entity id="492805" class="DrugOntology#prescription_
Selective and Non-Selective Non-Steroidal Anti-Inflamma
class="DrugOntology#prescription_drug_generic">NSAI

Today, the Food and Drug Administration (FDA) is annour
<Entity id="474305" class="DrugOntology#Organization"
to voluntarily withdraw <Entity id="122805" class="
DrugOntology#prescription_drug_brandname">Bextra
</Entity> (<Entity id="10288" class="DrugOntology#pre
valdecoxib</Entity>) from the market. Pfizer has agreed to
of Bextra in the <Entity id="7852" class="Sweto#country"
further discussions with the agency.
.....
This request is based on:
-Reports of serious and potentially life-threatening skin reactions, including deaths,
in patients using Bextra. The risk of these reactions in individual patients is unpredictable,
occurring in patients with and without a prior history of <Entity id="14280" class="
DrugOntology #interaction_with_physical_condition>sulfa allergy
</Entity>
.....
Date created: <Regexp type="date">April 7, 2005</Regexp>

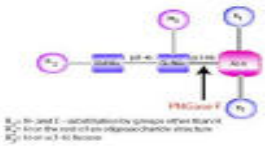
Excerpt of Drug Ontology

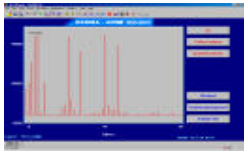


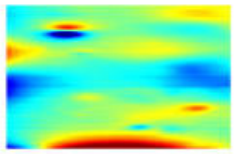
Sample Created Metadata

```
<Entity id="122805"
class="DrugOntology#prescription_drug_brandname">
Bextra
  <Relationship id="442134"
    class="DrugOntology#has_interaction">
    <Entity id="14280" class="DrugOntology
        #interaction_with_physical_condition>sulfa allergy
    </Entity>
  </Relationship>
</Entity>
```

N-Glycosylation Process (NGP)







Cell Culture

extract

Glycoprotein Fraction

proteolysis

Glycopeptides Fraction

1 — n

Separation technique I

Glycopeptides Fraction

PNGase

n

Peptide Fraction

Separation technique II

n*m

Peptide Fraction

Mass spectrometry

ms data

Data reduction

ms peaklist

binning

ms/ms data

Data reduction

ms/ms peaklist

Peptide identification

Peptide list

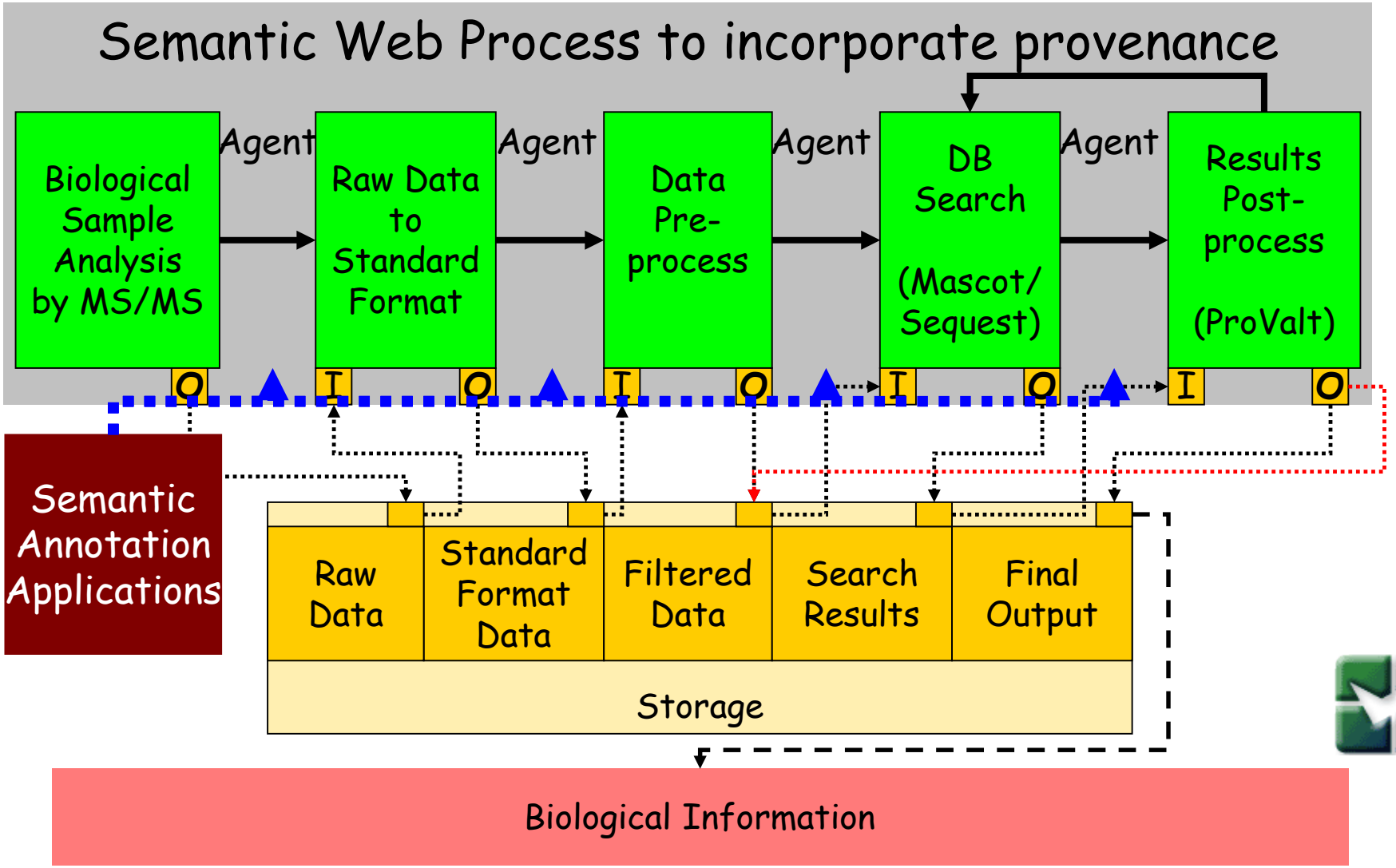
Data correlation

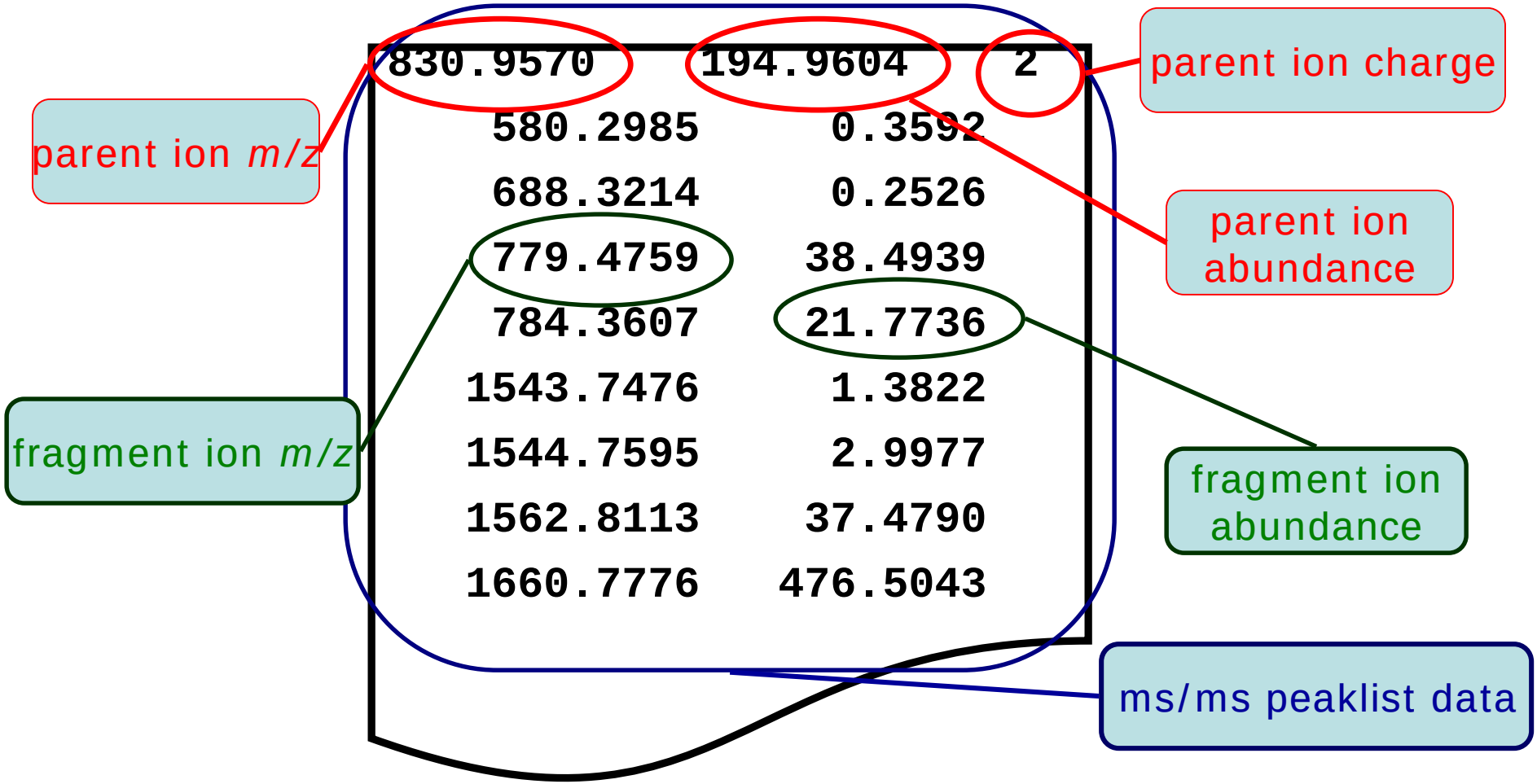
N-dimensional array

Signal integration

Glycopeptide identification and quantification

ISiS – Integrated Semantic Information and Knowledge System

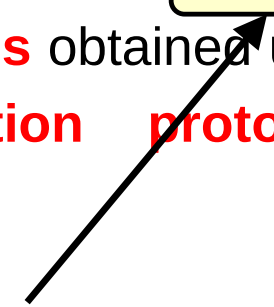




Mass Spectrometry (MS) Data

Semantic Annotation Facilitates Complex Queries

- *Evaluate the specific effects of changing a biological parameter:* Retrieve **abundance** data for a given **protein** expressed by three different **cell types** of a specific **organism**.
- *Retrieve raw data supporting a structural assignment:* Find all the **raw ms data files** that contain the **spectrum** of a given **peptide sequence** having a specific **modification** and **charge state**.
- *Detect errors:* Find and compare all **peptide** lists identified in **Mascot output files** obtained using a similar **organism**, **cell-type**, **sample preparation protocol**, and **mass spectrometry** conditions.



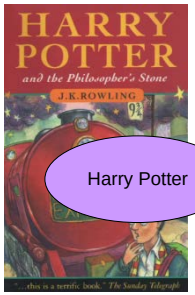
A Web Service
Must Be Invoked

ProPreO concepts highlighted in red

Example of Relevant Subgraph Discovery based on evidence

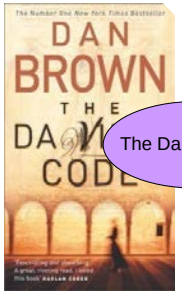
Anecdotal Example

UNDISCOVERED PUBLIC KNOWLEDGE
Discovering connections hidden in text



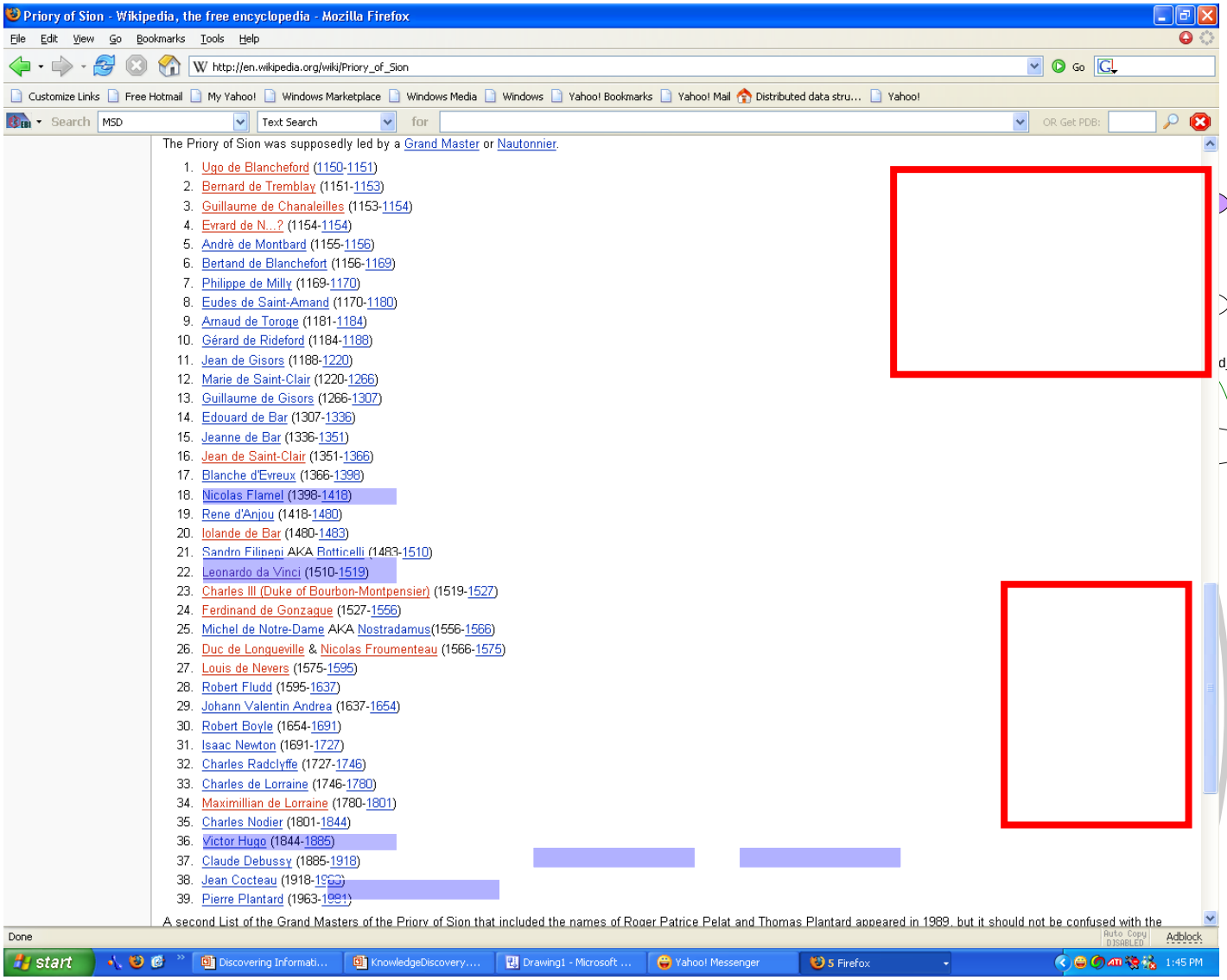
Harry Potter

Et in Arcadia Ego



The Da Vinci code

Santa Maria delle Grazie

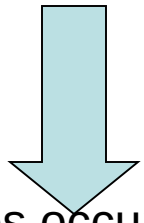

Priory of Sion - Wikipedia, the free encyclopedia - Mozilla Firefox
File Edit View Go Bookmarks Tools Help
http://en.wikipedia.org/wiki/Priory_of_Sion
The Priory of Sion was supposedly led by a Grand Master or Nautonnier.
1. Ugo de Blancheford (1150-1151)
2. Bernard de Tremblay (1151-1153)
3. Guillaume de Chanaleilles (1153-1154)
4. Evrard de N...? (1154-1154)
5. Andrè de Montbard (1155-1156)
6. Bertand de Blanchefort (1156-1169)
7. Philippe de Milly (1169-1170)
8. Eudes de Saint-Amand (1170-1180)
9. Arnaud de Toroge (1181-1184)
10. Gérard de Rideford (1184-1188)
11. Jean de Gisors (1188-1220)
12. Marie de Saint-Clair (1220-1266)
13. Guillaume de Gisors (1266-1307)
14. Edouard de Bar (1307-1336)
15. Jeanne de Bar (1336-1351)
16. Jean de Saint-Clair (1351-1366)
17. Blanche d'Evreux (1366-1398)
18. Nicolas Flamel (1398-1418)
19. Rene d'Anjou (1418-1480)
20. Iolande de Bar (1480-1483)
21. Sandro Filipepi AKA Botticelli (1483-1510)
22. Leonardo da Vinci (1510-1519)
23. Charles III (Duke of Bourbon-Montpensier) (1519-1527)
24. Ferdinand de Gonzague (1527-1556)
25. Michel de Notre-Dame AKA Nostradamus(1556-1566)
26. Duc de Longueville & Nicolas Froumenteau (1566-1575)
27. Louis de Nevers (1575-1595)
28. Robert Fludd (1595-1637)
29. Johann Valentin Andrea (1637-1654)
30. Robert Boyle (1654-1691)
31. Isaac Newton (1691-1727)
32. Charles Radclyffe (1727-1746)
33. Charles de Lorraine (1746-1780)
34. Maximillian de Lorraine (1780-1801)
35. Charles Nodier (1801-1844)
36. Victor Hugo (1844-1885)
37. Claude Debussy (1885-1918)
38. Jean Cocteau (1918-1963)
39. Pierre Plantard (1963-1991)
A second List of the Grand Masters of the Priory of Sion that included the names of Roger Patrice Pelat and Thomas Plantard appeared in 1989, but it should not be confused with the
Done
start
1:45 PM

Schema-Driven Extraction of Relationships from Biomedical Text

Cartic Ramakrishnan, Krys Kochut, Amit P. Sheth: A Framework for Schema-Driven Relationship Discovery from Unstructured Text. International Semantic Web Conference 2006: 583-596 [.pdf]

Method – Parse Sentences in PubMed

[1254239-1] An excessive endogenous or exogenous stimulation by estrogen induces adenomatous hyperplasia of the endometrium.



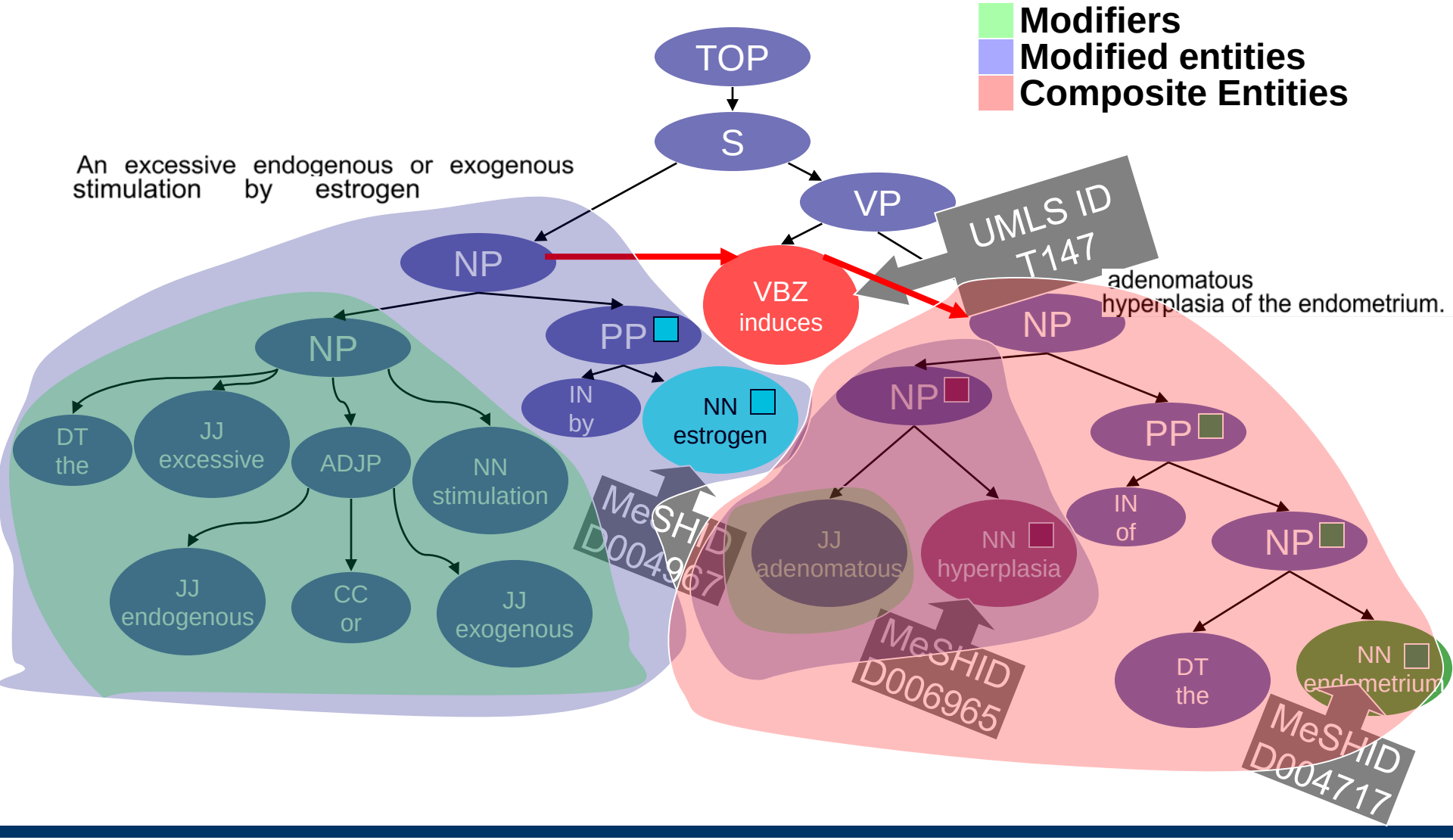
SS-Tagger (University of Tokyo)

SS-Parser (University of Tokyo)

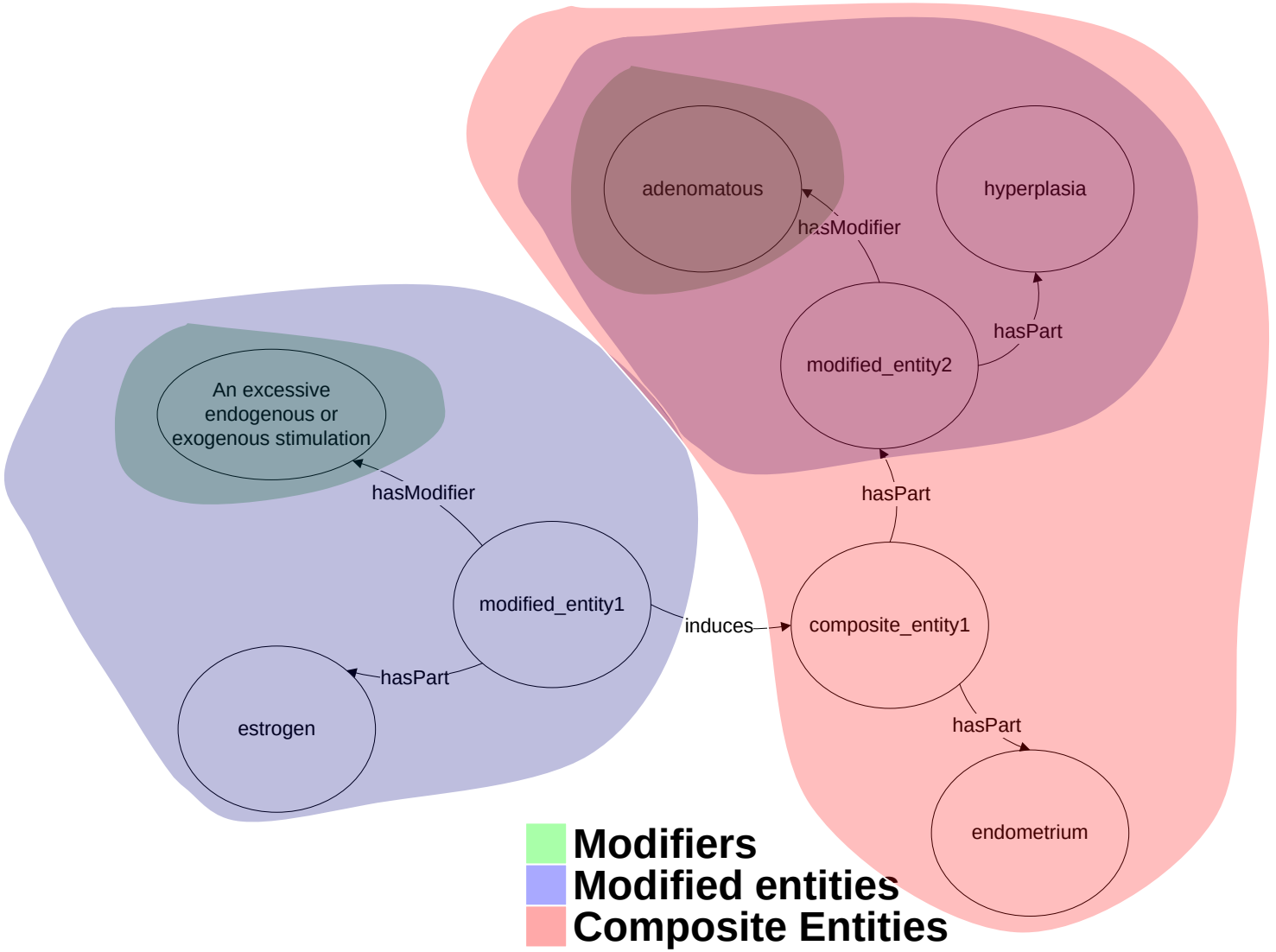
(TOP (S (NP (NP (DT An) (JJ excessive) (ADJP (JJ endogenous) (CC or) (JJ exogenous)) (NN stimulation)) (PP (IN by) (NP (NN estrogen))) (VP (VBZ induces) (NP (NP (JJ adenomatous) (NN hyperplasia)) (PP (IN of) (NP (DT the) (NN endometrium)))))))

- Entities (MeSH terms) in sentences occur in modified forms
  - "adenomatous" modifies "hyperplasia"
  - "An excessive endogenous or exogenous stimulation" modifies "estrogen"
- Entities can also occur as composites of 2 or more other entities
  - "adenomatous hyperplasia" and "endometrium" occur as "adenomatous hyperplasia of the endometrium"

Method – Identify entities and Relationships in Parse Tree

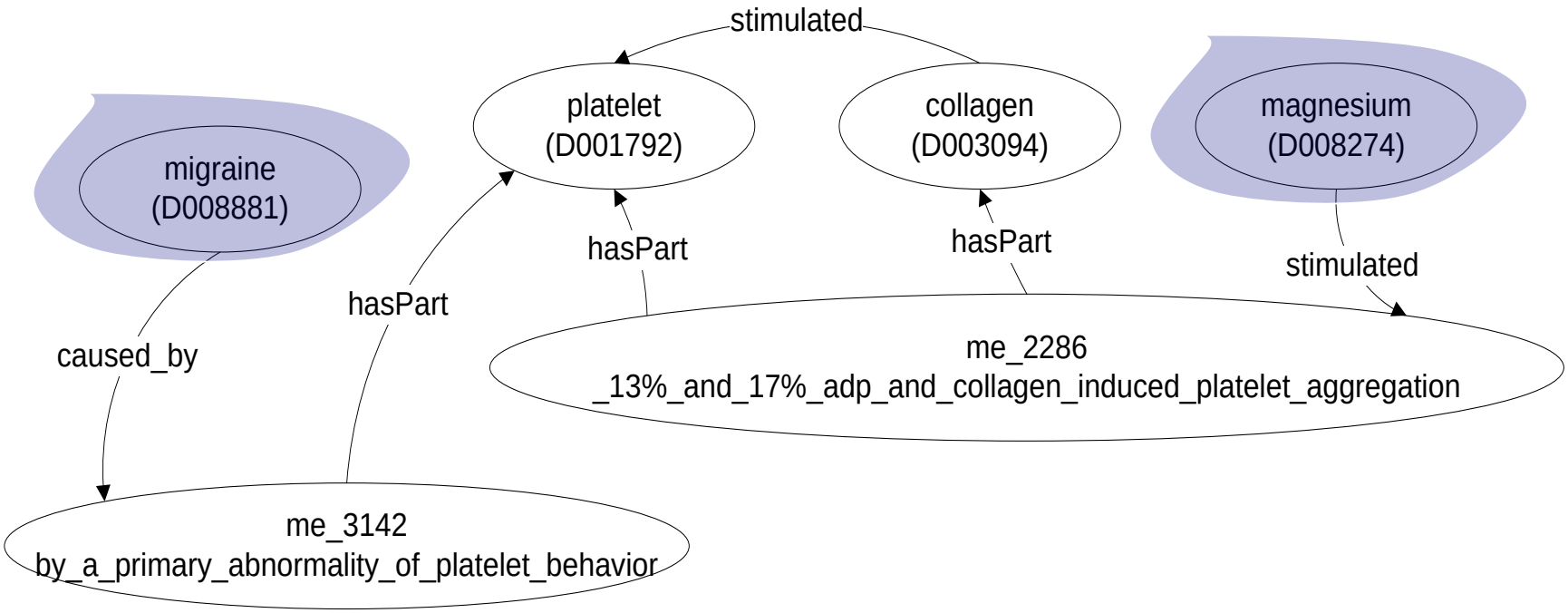


Resulting Semantic Web Data in RDF



Now possible – Extracting relationships between MeSH terms from PubMed

Once you have Semantic Web Data



QUESTION 1: Given an RDF graph without weights can we use domain knowledge to compute the strength of connection between any two entities?

QUESTION 2: Can we then compute the most "relevant" connections for a given pair of entities?

QUESTION 3: How many such connections can there be? Will this lead to a combinatorial explosion? Can the notion of relevance help?

- Problem: Discovering relevant connections between entities
  - All Paths problem is NP-Complete
  - Most informative paths are not necessarily the shortest paths

- Possible Solution: Heuristics-based Approach*
  - Find a smart, systematic way to weight the edges of the RDF graph so that the most important paths will have highest weight
  - Adopt algorithms for weighted graphs
    - Model graph as an electrical circuit† with weight representing conductance and find paths with highest current flow – i.e. top-k

* Cartic Ramakrishnan, William Milnor, Matthew Perry, Amit Sheth. "Discovering Informative Connection Subgraphs in Multi-relational Graphs", SIGKDD Explorations Special Issue on Link Mining, Volume 7, Issue 2, December 2005

† Christos Faloutsos, Kevin S. McCurley, Andrew Tomkins: Fast discovery of connection subgraphs. KDD 2004: 118-127

- What is a good path with respect to *knowledge discovery*?
  - Uses more specific classes and relationships
    - e.g. Employee vs. Assistant Professor
  - Uses rarer facts
    - Analogous to information gain
  - Involves unexpected connections
    - e.g. connects entities from different domains

- More specific classes and properties convey more information
- Specificity of property p_i:
  - $d(p_i)$ is the depth of p_i
  - $d(p_{iH})$ is the depth of the property hierarchy

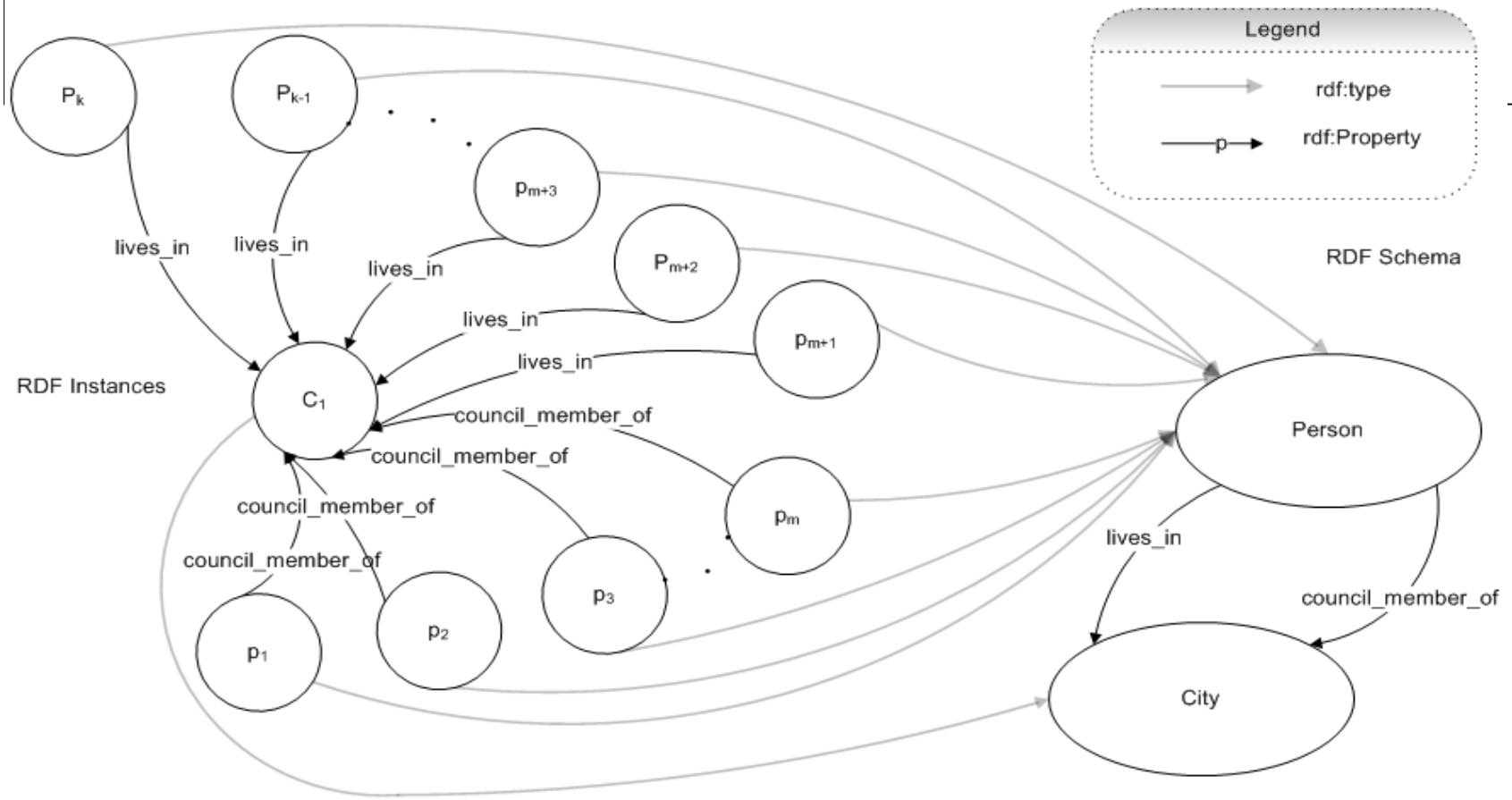
$$\mu(p_i) = \frac{d(p_i)}{d(p_{iH})}$$

- Specificity of class c_j:
  - $d(c_i)$ is the depth of c_j
  - $d(c_{iH'})$ is the depth of the class hierarchy

$$\mu(c_j) = \frac{d(c_j)}{d(c_{jH'})}$$

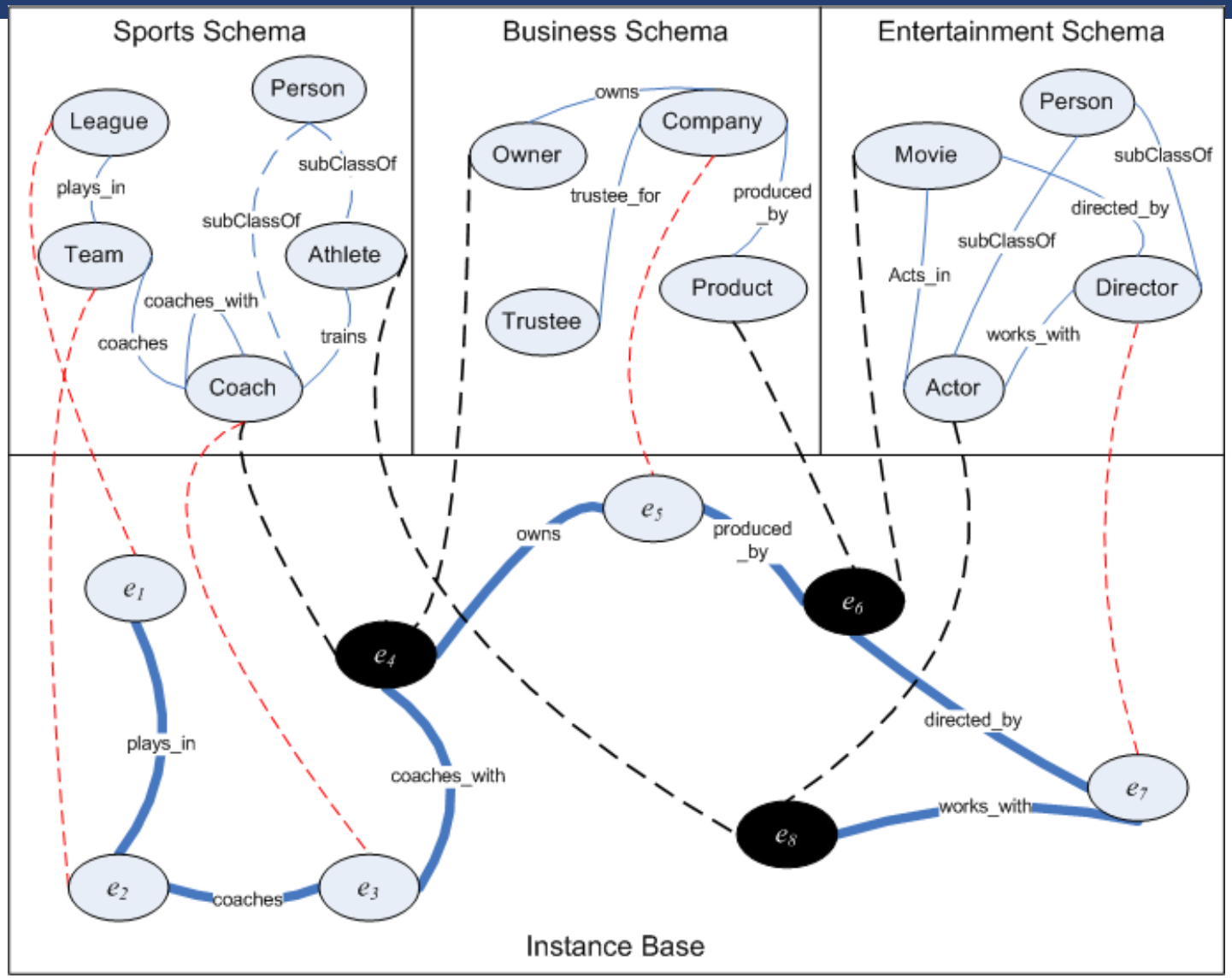
- *Node is weighted and this weight is propagated to edges incident to the node*

- Rare facts are more informative than frequent facts
- Define a *type* of an statement RDF <*s*,*p*,*o*>
  - Triple $\pi = <C_i, p_j, C_k>$
    - $typeOf(s) = C_i$
    - $typeOf(o) = C_k$
- $|\pi|$ = number of statements of type π in an RDF instance base
- *ISP* for a statement: $\sigma_\pi = 1/|\pi|$



- π = <*Person, lives_in, City*>
- π' = <*Person, council_member_of, City*>
- $\sigma_\pi = 1/(k-m)$ *and* $\sigma_{\pi'} = 1/m$, *and if* $k-m>m$ *then* $\sigma_{\pi'} > \sigma_\pi$

- RDF allows Multiple classification of entities
  - Possibly classified in different schemas
  - Tie different schemas together
- *Refraction* is Indicative of anomalous paths
- SPAN favors *refracting* paths
  - Give extra weight to multi-classified nodes and propagate it to the incident edges


Sports Schema
Business Schema
Entertainment Schema
Person
League
subClassOf
plays_in
subClassOf
Team
Athlete
coaches_with
coaches
trains
Coach
owns
Company
Owner
trustee_for
produced_by
Product
Trustee
Person
Movie
subClassOf
directed_by
subClassOf
Acts_in
Director
works_with
Actor
owns
produced_by
directed_by
plays_in
coaches_with
works_with
coaches
Instance Base

- What if we are not just interested in knowledge discovery style searches?
- Can we provide a mechanism to adjust relevance measures with respect to users' needs?
  - ~~Conventional Search vs. Discovery Search~~

Yes! ... SemRank*

* Kemafor Anyanwu, Angela Maduko, Amit Sheth. "SemRank: Ranking Complex Relationship Search Results on the Semantic Web", The 14th International World Wide Web Conference, (WWW2005), Chiba, Japan, May 10-14, 2005

QUERY PROCESSOR

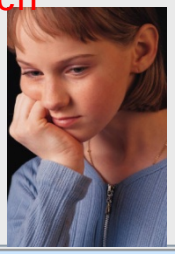
LSDIS
Large Scale Distributed Information Systems

SSARK

SSARK

Semantic Searching of a DiffeRent Kind

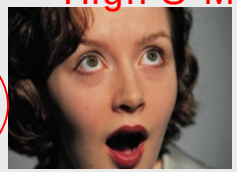
Low Information Gain
Low Refraction Count
High S-Match



Query Specification

Select Search Mode: 50 %

Conventional — Discovery



High Information Gain
High Refraction Count
High S-Match

adjustable search mode

Enter the two resources

SWEET_198959 SWEET_307295

Relevance Specification (seperated with spaces)

Search | Reset | Close | Previous | Next

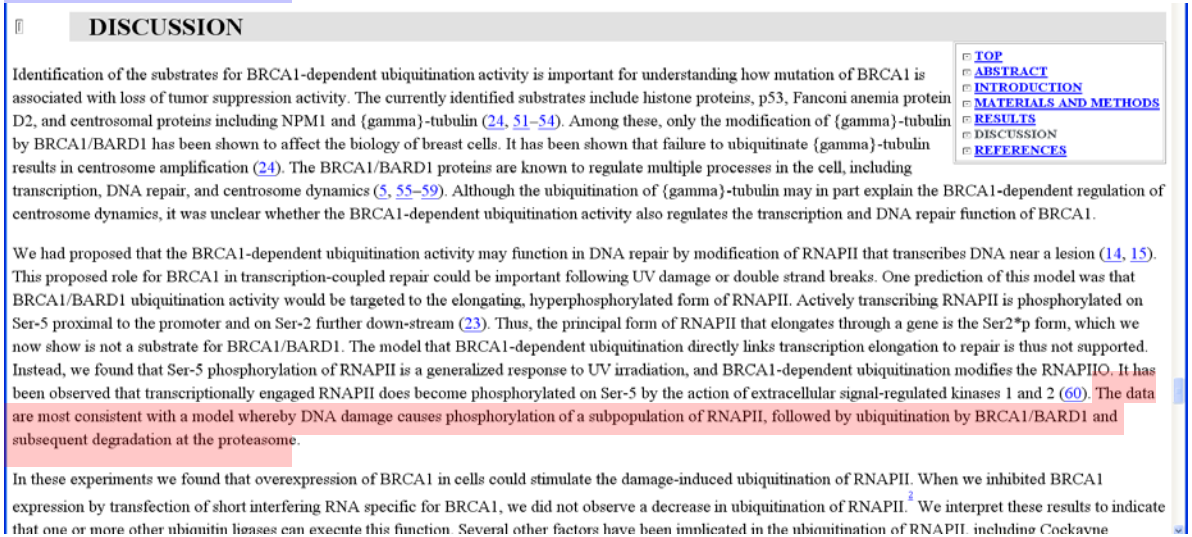
Blazing Semantic Trails in Biomedical Literature

Cartic Ramakrishnan, Amit P. Sheth: Blazing Semantic Trails in Text: Extracting Complex Relationships from Biomedical Literature. Tech. Report #TR-RS2007 [.pdf]

"The physician, puzzled by her patient's reactions, strikes the trail established in studying an earlier similar case, and runs rapidly through analogous case histories, with side references to the classics for the pertinent anatomy and histology. The chemist, struggling with the synthesis of an organic compound, has all the chemical literature before him in his laboratory, with trails following the analogies of compounds, and side trails to their physical and chemical behavior." [V. Bush, As We May Think. The Atlantic Monthly, 1945. 176(1): p. 101-108.]

Original documents

PMID-15886201



DISCUSSION

TOP
ABSTRACT
INTRODUCTION
MATERIALS AND METHODS
RESULTS
DISCUSSION
REFERENCES

Identification of the substrates for BRCA1-dependent ubiquitination activity is important for understanding how mutation of BRCA1 is associated with loss of tumor suppression activity. The currently identified substrates include histone proteins, p53, Fanconi anemia protein D2, and centrosomal proteins including NPM1 and {gamma}-tubulin (24, 51–54). Among these, only the modification of {gamma}-tubulin by BRCA1/BARD1 has been shown to affect the biology of breast cells. It has been shown that failure to ubiquitinate {gamma}-tubulin results in centrosome amplification (24). The BRCA1/BARD1 proteins are known to regulate multiple processes in the cell, including transcription, DNA repair, and centrosome dynamics (5, 55–59). Although the ubiquitination of {gamma}-tubulin may in part explain the BRCA1-dependent regulation of centrosome dynamics, it was unclear whether the BRCA1-dependent ubiquitination activity also regulates the transcription and DNA repair function of BRCA1.

We had proposed that the BRCA1-dependent ubiquitination activity may function in DNA repair by modification of RNAPII that transcribes DNA near a lesion (14, 15). This proposed role for BRCA1 in transcription-coupled repair could be important following UV damage or double strand breaks. One prediction of this model was that BRCA1/BARD1 ubiquitination activity would be targeted to the elongating, hyperphosphorylated form of RNAPII. Actively transcribing RNAPII is phosphorylated on Ser-5 proximal to the promoter and on Ser-2 further down-stream (23). Thus, the principal form of RNAPII that elongates through a gene is the Ser2*p form, which we now show is not a substrate for BRCA1/BARD1. The model that BRCA1-dependent ubiquitination directly links transcription elongation to repair is thus not supported. Instead, we found that Ser-5 phosphorylation of RNAPII is a generalized response to UV irradiation, and BRCA1-dependent ubiquitination modifies the RNAPIIO. It has been observed that transcriptionally engaged RNAPII does become phosphorylated on Ser-5 by the action of extracellular signal-regulated kinases 1 and 2 (60). The data are most consistent with a model whereby DNA damage causes phosphorylation of a subpopulation of RNAPII, followed by ubiquitination by BRCA1/BARD1 and subsequent degradation at the proteasome.

In these experiments we found that overexpression of BRCA1 in cells could stimulate the damage-induced ubiquitination of RNAPII. When we inhibited BRCA1 expression by transfection of short interfering RNA specific for BRCA1, we did not observe a decrease in ubiquitination of RNAPII.[2] We interpret these results to indicate that one or more other ubiquitin ligases can execute this function. Several other factors have been implicated in the ubiquitination of RNAPII, including Cockayne

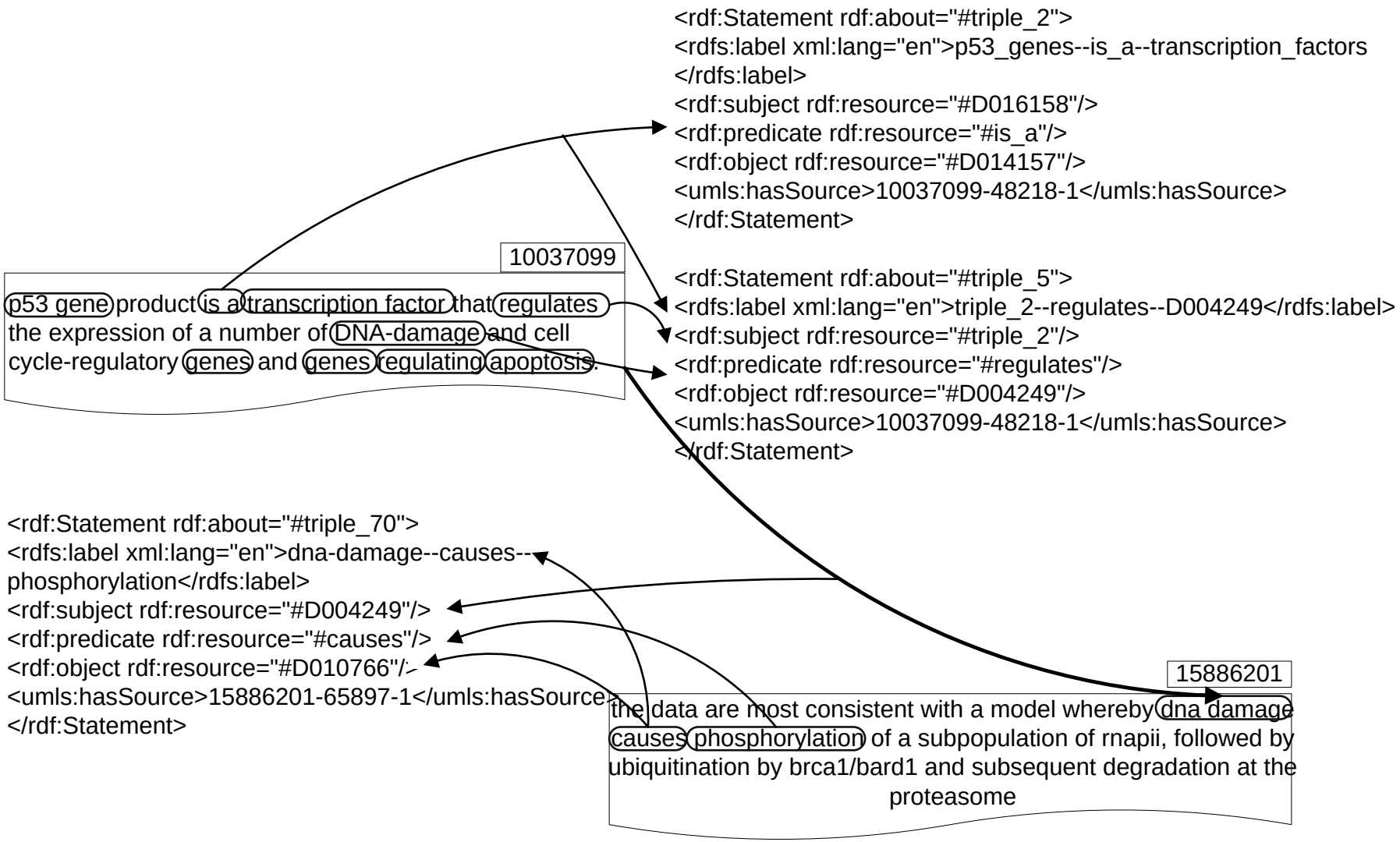
PMID-10037099

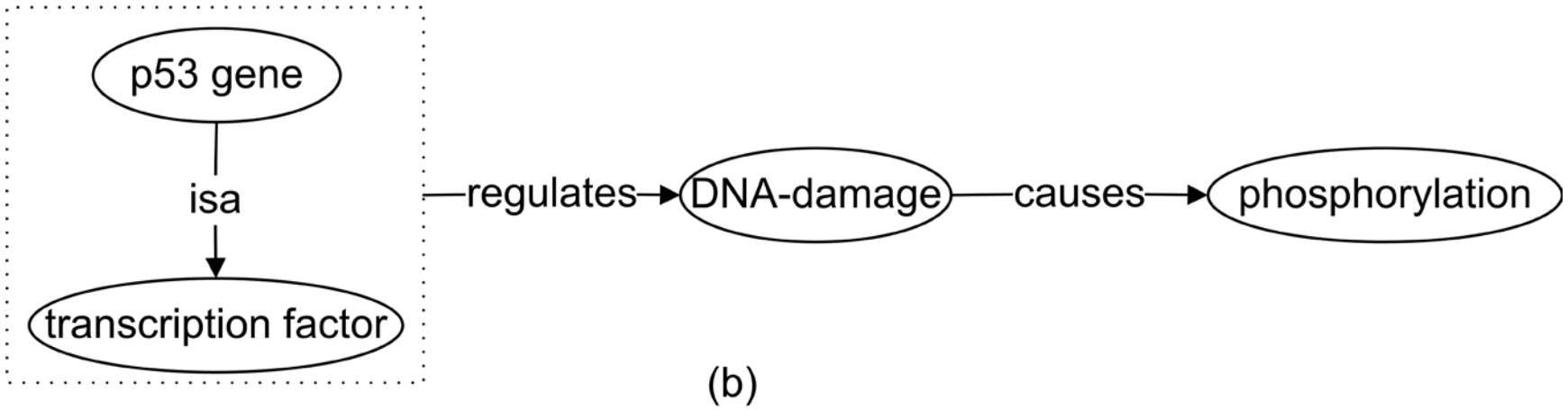
In the mouse two-stage skin carcinogenesis model, tumor promotion is a distinct, rate-limiting step that determines the formation of premalignant tumors. As discussed above, the role of tumor promoters in human cancer is more complex because human exposure tends to involve sporadic low doses of complex mixtures of carcinogens, co-carcinogens, and tumor-promoting agents. Nonetheless, studies of rodent tumor models of liver, bladder, colon, and breast cancers—and analyses of human tumor formation—suggest that processes analogous to tumor promotion by TPA on the mouse skin are a common feature of carcinogenesis (1). Thus, epigenetic changes in cell signaling, such as altered growth factor production and receptor expression, and elevated synthesis of inflammatory and mitogenic factors, such as cytokines and eicosanoids, are key targets for inhibiting tumor promotion.

Tumor Progression

As noted earlier, tumor progression involves the accumulation of additional genetic alterations in an initiated cell clone and generally gives a growth advantage to the progressing clone. In progression, a focal lesion consisting of a population of initiated and promoted cells ultimately becomes an invasive malignant tumor. One frequently observed genetic alteration that appears to contribute to malignant progression is mutation in the p53 [also known as TP53] tumor suppressor gene (62). The p53 gene product is a transcription factor that regulates the expression of a number of DNA-damage and cell cycle-regulatory genes and genes regulating apoptosis. By enhancing transcription of these critical genes, p53 regulates the cellular response to DNA damage (63). p53 also plays a role in maintaining genomic stability (64). Genomic instability, a hallmark of spontaneous malignant progression, is characterized by sequential chromosomal aberrations, such as duplications, deletions, and loss of

Complex relationships connecting documents – Semantic Trails




p53 gene
isa
transcription factor
regulates
DNA-damage
causes
phosphorylation

(b)

Semantic Trails can be built over a Web of Semantic (Meta)Data

extracted (manually, semi-automatically and automatically) and gleaned from

- Structured data (e.g., NCBI databases)
- Semi-structured data (e.g., XML based and semantic metadata standards for domain specific data representations and exchanges)
- Unstructured data (e.g., Pubmed and other biomedical literature)

and

- Various modalities (experimental data, medical images, etc.)

Semantic Metadata can be extracted from unstructured (eg, biomedical literature), semi-structured (eg, some of the Web content), structured (eg, databases) data and data of various modalities (eg, sensor data, biomedical experimental data). Focusing on the relationships and the web of their interconnections over entities and facts (knowledge) implicit in data leads to a Relationship Web.

Relationship Web takes you away from "which document" could have information I need, to "what's in the resources" that gives me the insight and knowledge I need for decision making.

Amit P. Sheth, Cartic Ramakrishnan: Relationship Web: Blazing Semantic Trails between Web Resources. IEEE Internet Computing, July 2007.

Demonstration of Semantic Trailblazing using a Semantic Browser

This application demonstrating use of ontology-supported relationship extraction (represented in RDF) and their traversal in context (as deemed relevant by the scientists), linking parts of knowledge represented in one biomedical document (currently a sentence in an abstract in Pubmed) to parts of knowledge represented in another document.

This is a prototype and lot more work remains to be done to build a robust system that can support Semantic Trailblazing. For more information:

Cartic Ramakrishnan, Krys Kochut, Amit P. Sheth: A Framework for Schema-Driven Relationship Discovery from Unstructured Text. International Semantic Web Conference 2006: 583-596 [.pdf]

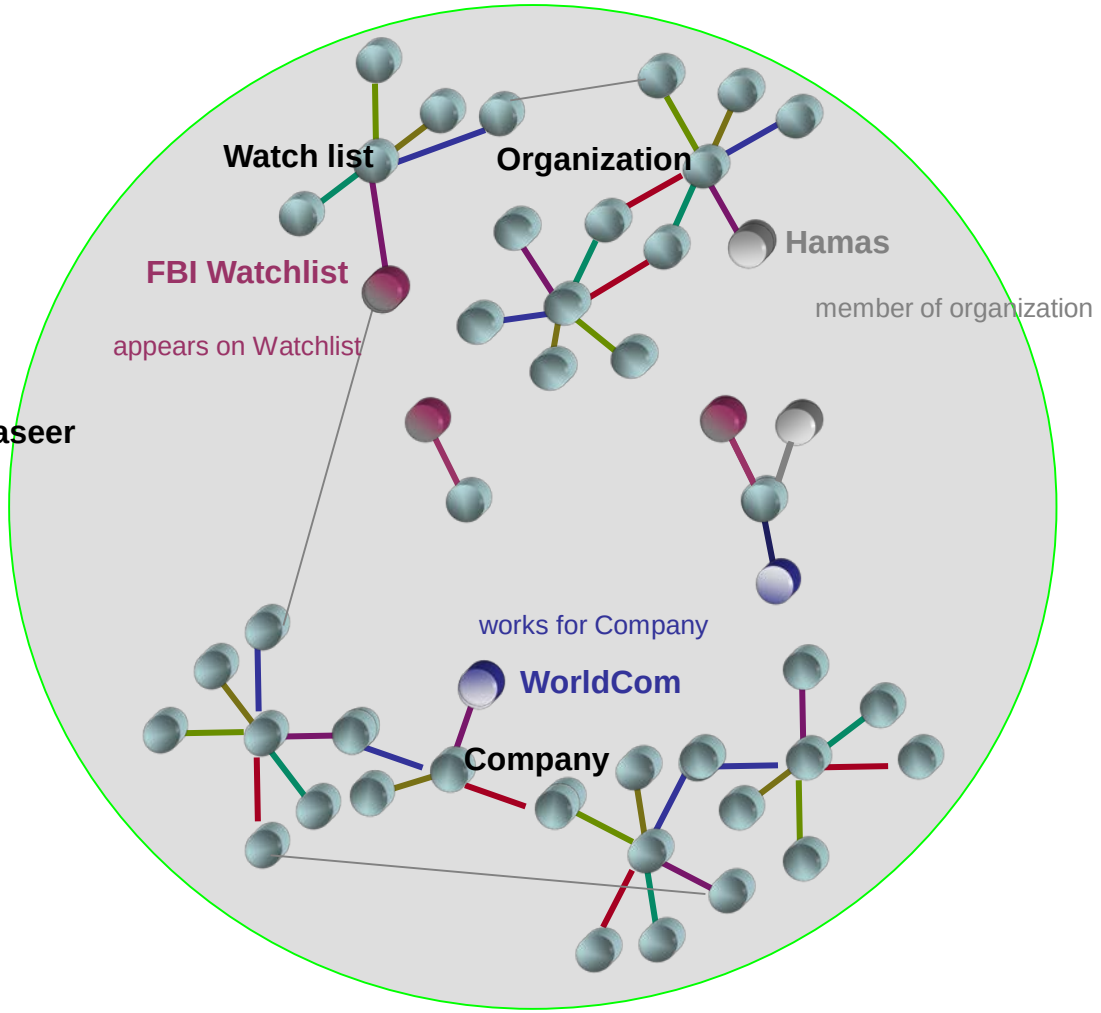
Cartic Ramakrishnan, Amit P. Sheth: Blazing Semantic Trails in Text: Extracting Complex Relationships from Biomedical Literature. Tech. Report #TR-RS2007 [.pdf]

Applications

“Everything's connected, all along the line. Cause and effect.
That's the beauty of it.
Our job is to trace the connections and reveal them.”
Jack in Terry Gilliam’s 1985 film - “Brazil”

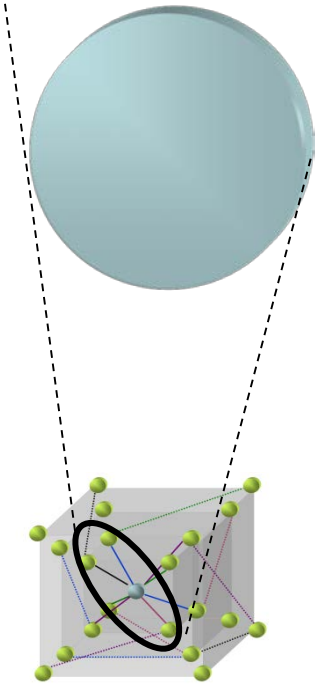
An application in Risk & Compliance

Ahmed Yaseer



Ahmed Yaseer:

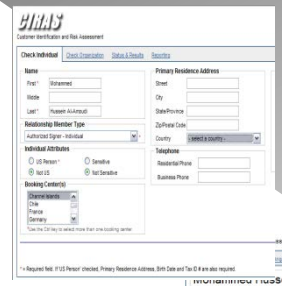
- *Appears on Watchlist 'FBI'*
- *Works for Company 'WorldCom'*
- *Member of organization 'Hamas'*

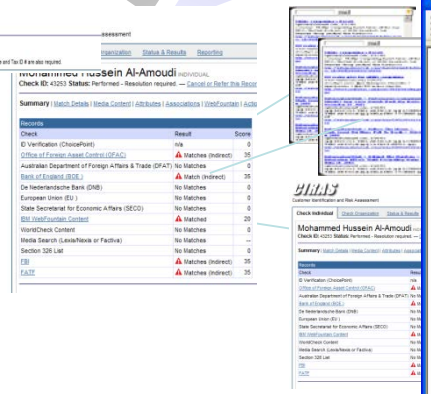


Semi-structured Government Data

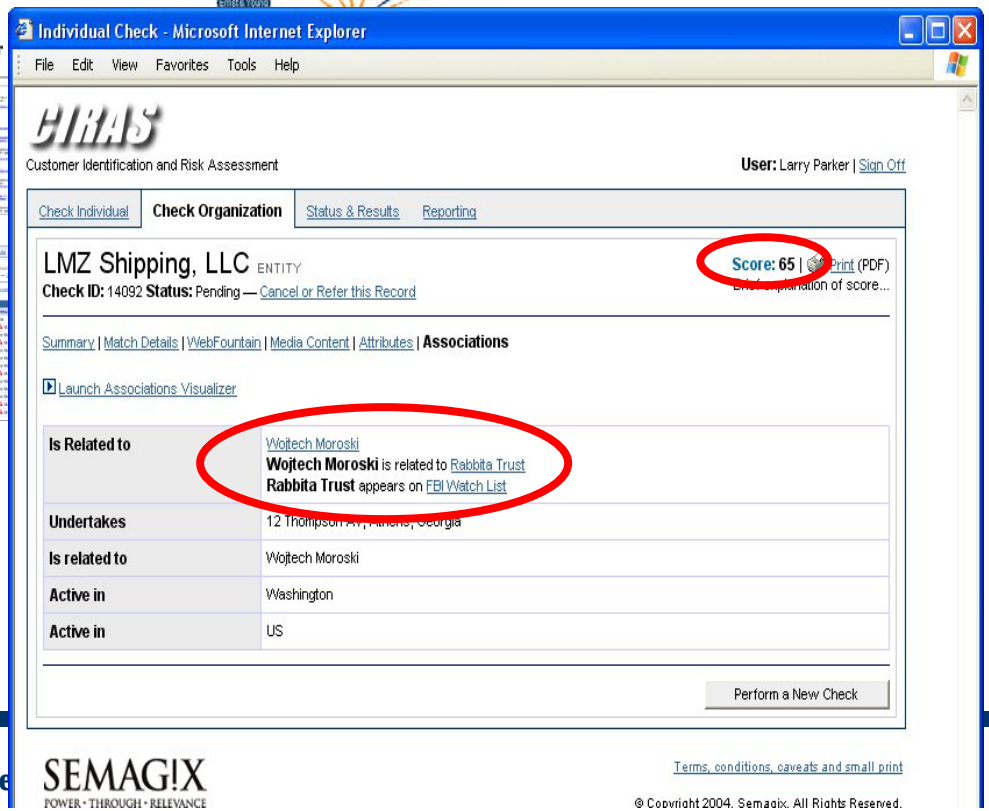
Un-structure text, Semi-structured Data

Establishing New Account





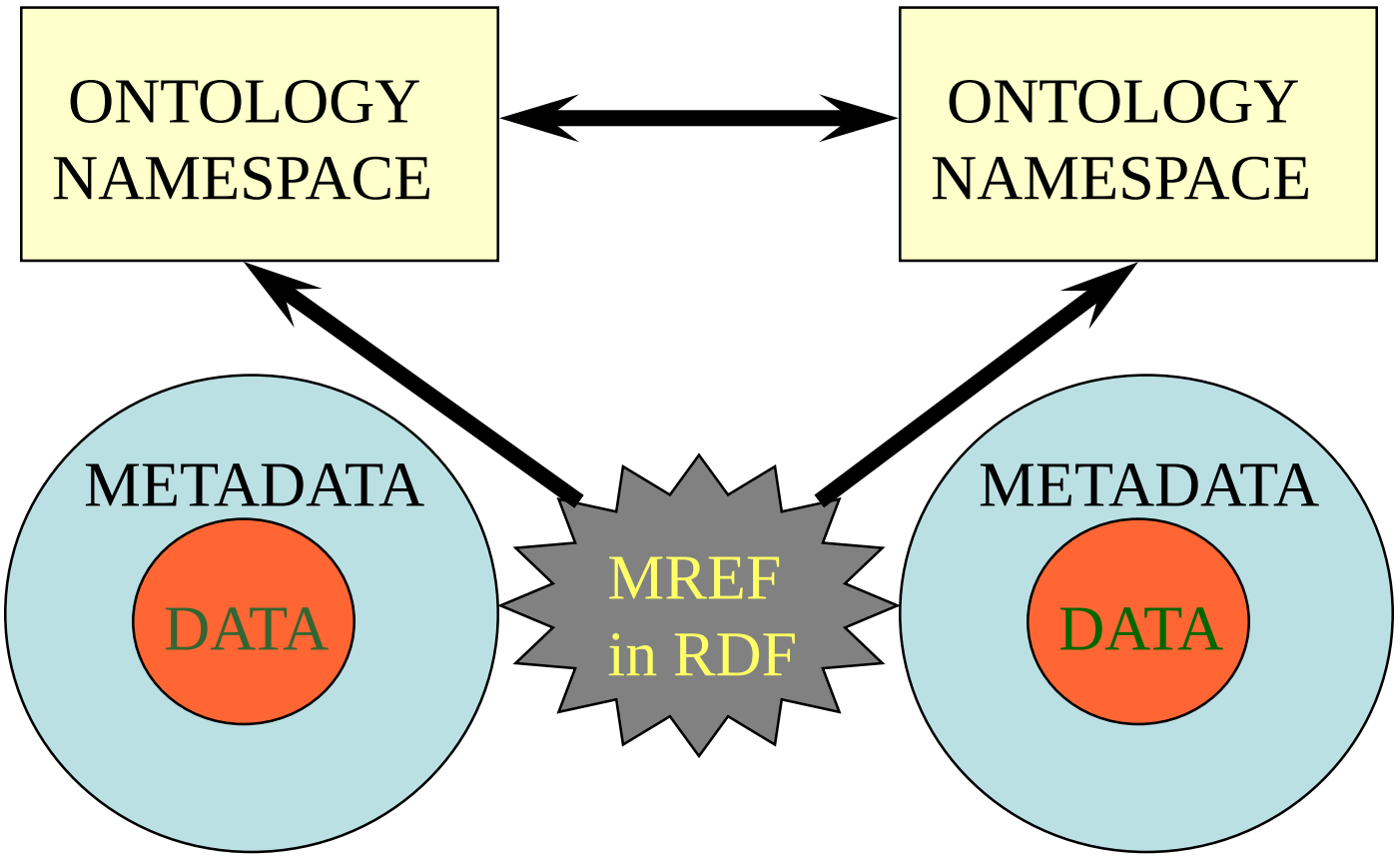
Scores the entity based on the content and entity relationships



Example of Fraud prevention application used in financial services

Creating “logical web” through

Media Independent Metadata based Correlation

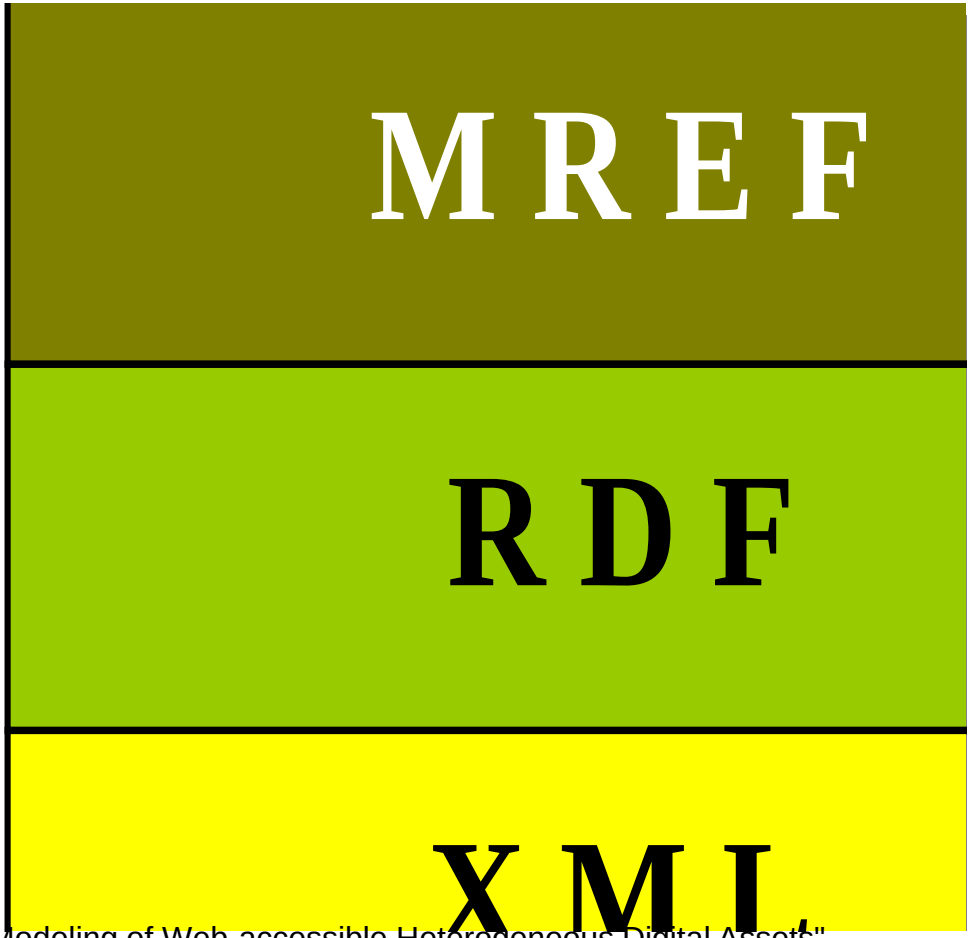


MREF (1998)

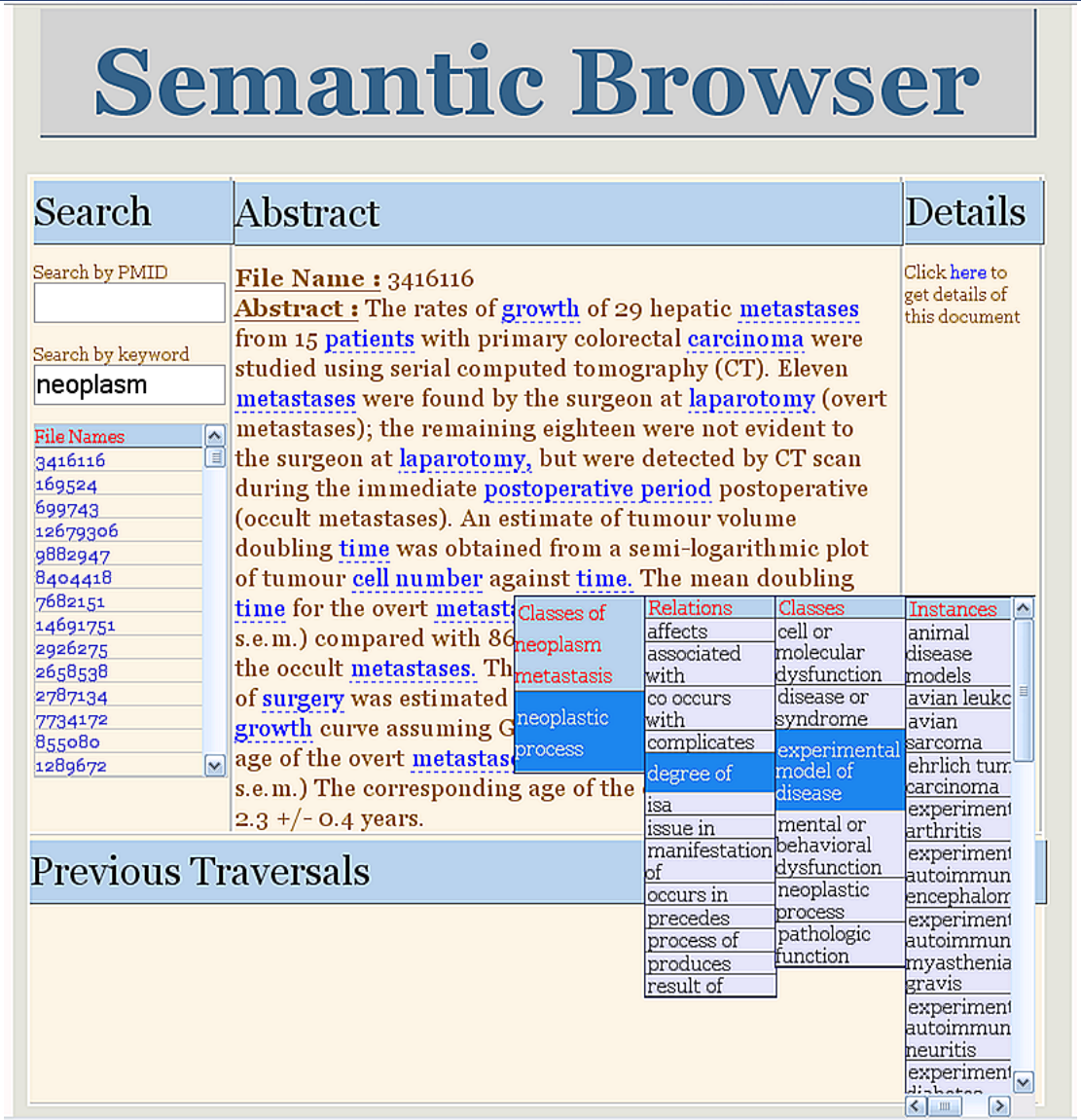
Model for Logical Correlation using Ontological Terms and Metadata

Framework for Representing MREFs

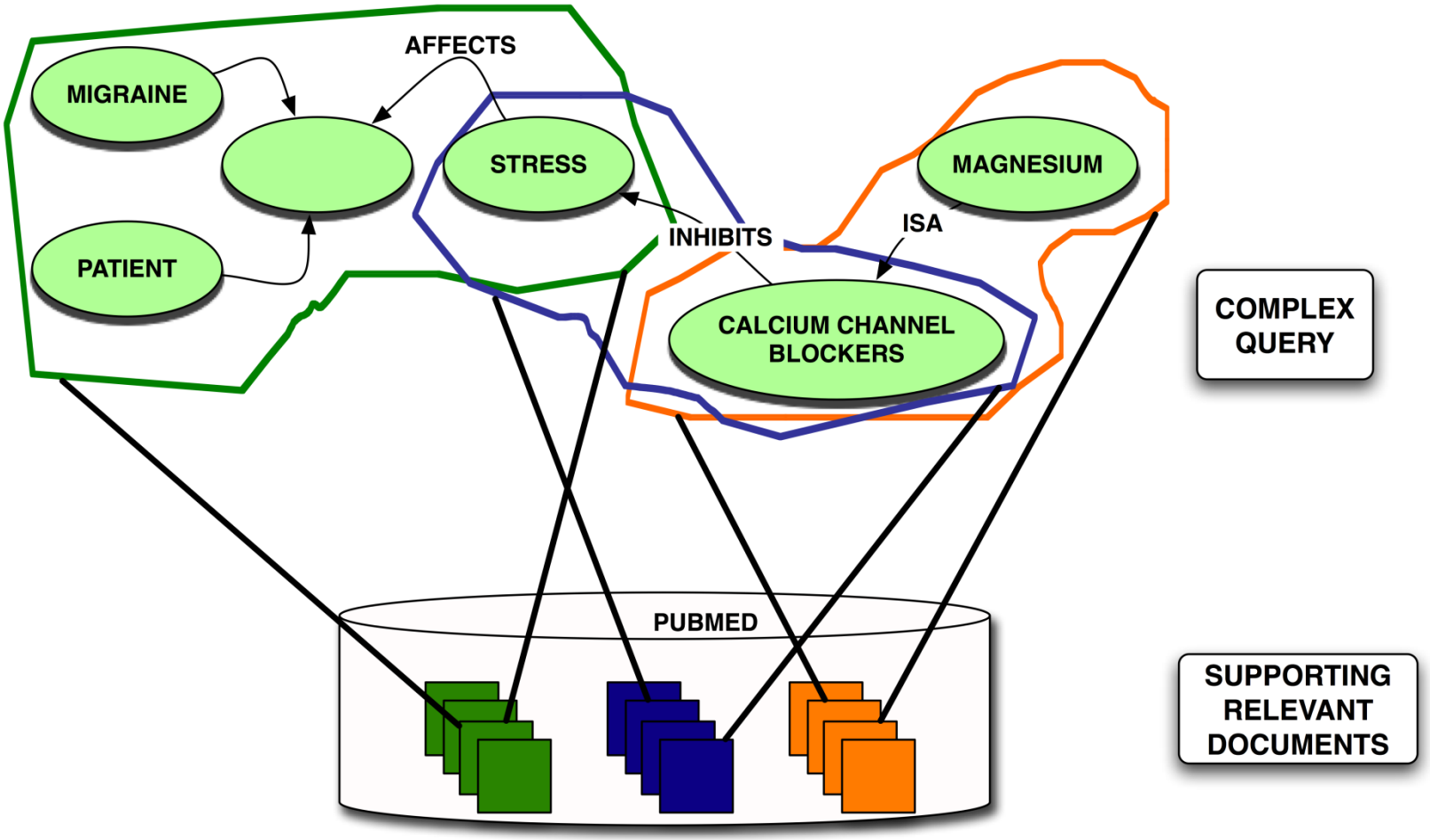
Serialization (one implementation choice)



K. Shah and A. Sheth, "Logical Information Modeling of Web-accessible Heterogeneous Digital Assets", Proc. of the Forum on Research and Technology Advances in Digital Libraries," (ADL'98), Santa Barbara, CA, May 28-30, 1998, pp. 266-275.


Semantic Browser
Search
Search by PMID
Search by keyword
neoplasm
File Names
3416116
169524
699743
12679306
9882947
8404418
7682151
14691751
2926275
2658538
2787134
7734172
855080
1289672
Abstract
File Name : 3416116
Abstract : The rates of growth of 29 hepatic metastases from 15 patients with primary colorectal carcinoma were studied using serial computed tomography (CT). Eleven metastases were found by the surgeon at laparotomy (overt metastases); the remaining eighteen were not evident to the surgeon at laparotomy, but were detected by CT scan during the immediate postoperative period postoperative (occult metastases). An estimate of tumour volume doubling time was obtained from a semi-logarithmic plot of tumour cell number against time. The mean doubling time for the overt metast
s.e.m.) compared with 86
the occult metastases. Th
of surgery was estimated
growth curve assuming G
age of the overt metastas
s.e.m.) The corresponding age of the
2.3 +/- 0.4 years.
Details
Click here to get details of this document
Classes of
neoplasm
metastasis
neoplastic process
Relations
affects
associated with
co occurs with
complicates
degree of
isa
issue in
manifestation of
occurs in
precedes
process of
produces
result of
Classes
cell or molecular dysfunction
disease or syndrome
experimental model of disease
mental or behavioral dysfunction
neoplastic process
pathologic function
Instances
animal disease models
avian leuko
avian sarcoma
ehrlich tum
carcinoma
experiment
arthritis
experiment
autoimmun
encephalom
experiment
autoimmun
myasthenia
gravis
experiment
autoimmun
neuritis
experiment
Previous Traversals

Hypothesis driven retrieval of Scientific Text



Relationship Web takes you away from “which document” could have information I need, to “what’s in the resources” that gives me the insight and knowledge I need for decision making.

Amit P. Sheth, Cartic Ramakrishnan: Relationship Web: Blazing Semantic Trails between Web Resources. IEEE Internet Computing July 2007 (to appear) [.pdf]

World class research center- coupled with daytaOhio for tech transfer and commercialization

Core expertise in

- data management: integration, mining, analytics, visualization
- distributed computing: services/grid computing
- Semantic Web
- Bioinformatics, etc.

With domain/application expertise in Government, Industry, Biomedicine

Member of World Wide Web Consortium and extensive industry relationships

Core expertise in

- data management: integration, mining, analytics, visualization
- distributed computing: services/grid computing
- Semantic Web
- Bioinformatics, etc.

With domain/application expertise in Government, Industry, Biomedicine

W3C member, extensive industry relationships

http://knoesis.wright.edu